Project Information

HGS Code	25750
Template ID	HTPAN08
Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Nucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
       (1863 letters, both strands)

Database: nt
          162,249 sequences; 174,644,254 total letters.
Searching..done

		High Score	Smallest Poisson Probability P(N)	N
gb|X55448|HSG6PDGEN	Human complete G6PD gene for glucose-...	1029	2.9e-104	2
gb|K03021|HUMTPA	Human tissue plasminogen activator (t...	830	2.0e-100	2
gb|M26434|HUMHPRTB	Human hypoxanthine phosphoribosyltran...	830	4.6e-94	2
gb|T10601|T10601	hbc778 Homo sapiens cDNA clone hbc778...	1140	9.2e-87	1
gb|D00591|HUMRCC1	Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1	H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078	EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3	H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467	H.sapiens HLA class III DNA	829	1.2e-82	2
gb|L10641|HUMVTDBP	Human vitamin D-binding protein (GC) ...	721	1.4e-81	2

>gb\|X55448\|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
    dehydrogenase >gb\|Z29527\|HSG6PHDH H.sapiens G6PD gene for
    glucose-6-phosphate dehydrogenase
    Length = 52,173

  Plus Strand HSPs:

  Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
  Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

Query: 1570 TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
              ||||| | | || || || |||||||||||||| |||||||||| || ||||||
Sbjct: 5032 TAAAATACAAAAATTGGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091

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gb|D00591|HUMRCC1 Human RCC1 gene, complete cds.	577	3.3e-85	3
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gb|M79078|M79078 EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3 H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467 H.sapiens HLA class III DNA	829	1.2e-82	2
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        Length = 52,173

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             |||||| | | || || || ||||||||||||| |||||||||||| || |||||
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gb|D00591|HUMRCC1	Human RCC1 gene, complete cds.	577	3.3e-85	3
gb|X69907|HSATPCP1	H.sapiens gene for mitochondrial ATP ...	618	2.3e-84	3
gb|M79078|M79078	EST01226 Homo sapiens cDNA clone HHCP...	1099	1.8e-83	1
gb|X68793|HSAT3	H.sapiens gene for antithrombin III	633	5.2e-83	2
gb|Z15027|HSHLA1467	H.sapiens HLA class III DNA	829	1.2e-82	2
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>gb\|X55448\|HSG6PDGEN Human complete G6PD gene for glucose-6-phosphate
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    Length = 52,173

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             ||||| | | || || || |||||||||||||| |||||||||| || ||||||
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Library	Human Pancreas Tumor
Project Name	fas ligand
Created By	Steve Ruben
Date Created	2/2/94

Nucleotide BLAST Analysis

Neucleotide Blast of HTPAN08 Full Contig + Screens

Query= HTPAN08XX   HGS #285507
        (1863 letters, both strands)

Database: nt
            162,249 sequences; 174,644,254 total letters.
Searching...done

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Poisson Probability P(N)	N
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gb|K03021|HUMTPA	Human tissue plasminogen activator (t...	830	2.0e-100	2
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gb|Z15027|HSHLA1467	H.sapiens HLA class III DNA	829	1.2e-82	2
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        Length = 52,173

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Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

```
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              ||||| |    | || ||  || ||||||||||||| |||||||||| || ||||||
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    Length = 52,173

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        dehydrogenase >gb|Z29527|HSG6PHDH H.sapiens G6PD gene for
        glucose-6-phosphate dehydrogenase
        Length = 52,173

    Plus Strand HSPs:

    Score = 1029 (284.3 bits), Expect = 4.0e-75, P = 4.0e-75
    Identities = 245/294 (83%), Positives = 245/294 (83%), Strand = Plus

Query: 1570 TAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGAA 1629
             ||||| |. | || || || ||||||||||||||||| |||||||||||| || ||||||
Sbjct: 5032 TAAAATACAAAAATTGGCTGGGCGCAGTGGCTCACATCTGTAATCCCAGCACTTTGGGGG 5091

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Query:   1630 CCCAAGGTGGGTAGATCACGAGATCAAGAGATCAAGACCATAGTGACCAACATAGTGAAA 1689
              |||||||||| ||||||| || |||||||||| |||||| || ||||||| ||||||
Sbjct:   5092 GCCAAGGTGGGCAGATCACAAGGTCAAGAGATCGAGACCATCCTGGCCAACATGGTGAAA 5151

Query:   1690 CCCCATCTCTACTGAAAGTGCAAAAATTAGCTGGGTGTGTTGGCACATGCCTGTAGTCCC 1749
              |||||||||||| ||| | |||||||||||||||| ||| ||| | ||||||||||||
Sbjct:   5152 CCCCATCTCTACTAAAAATACAAAAATTAGCTGGGCGTGGTGGTGCGTGCCTGTAGTCCC 5211

Query:   1750 AGCTACTTGAGAGGCTGAGGCAGGAGAATCGTTTGAACCCGGGAGGCAGAGGTTGCAGTG 1809
              |||||||      ||||||||||| ||||||| |||||| | ||||| ||||||||||||
Sbjct:   5212 AGCTACTCAGTAGGCTGAGGCAGTAGAATCGCTTGAATCAGGGAGTCAGAGGTTGCAGTG 5271

Query:   1810 TGGTGAGATCATGCCACTACACTCCAGCCTGGCGACAGAGCGAGACTTGGTTTC 1863
              | ||||||| |||||| |||||||||||||||||||||||||||||||| || ||
Sbjct:   5272 AGCTGAGATCGCGCCACTGCACTCCAGCCTGGCGACAGAGCGAGACTCTGTCTC 5325
```

    Score = 133 (36.8 bits), Expect = 1.9, P = 0.85
    Identities = 53/86 (61%), Positives = 53/86 (61%), Strand = Plus

```
Query:   1569 CTAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGGA 1628
              || |||| |    | || ||| || | |||| | | |||||||||||| | ||||||
Sbjct:  34625 CTCAAAAAAAAAAAATTAGCCAGGCACGGTGGTGCGCGCCTGTAATCCCAGCTACTTGGGA 34684

Query:   1629 ACCCAAGGTGGGTAGATCACGAGATC 1654
              | ||| || ||| | || |
Sbjct:  34685 GGCTGAGGCAGGAGAATCGCTTGAAC 34710
```

    Score = 126 (34.8 bits), Expect = 0.0019, Poisson P(2) = 0.0019
    Identities = 50/81 (61%), Positives = 50/81 (61%), Strand = Plus

```
Query:   1568 ACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACATTTTGGG 1627
              || |||| |     |   | |  || || | | |||  || ||||||||||||| ||||||
Sbjct:     53 ACAAAAAAAAAAAAAAATAGCTGGGAGTGATGGTGCATGCCTGTAATCCCAGCTATTTGGG 112

Query:   1628 AACCCAAGGTGGGTAGATCAC 1648
              || | ||| || || ||| |
Sbjct:    113 AAGCTGAGGCAGGAGAATCGC 133
```

    Minus Strand HSPs:

    Score = 888 (245.4 bits), Expect = 2.3e-63, P = 2.3e-63
    Identities = 220/273 (80%), Positives = 220/273 (80%), Strand = Minus

```
Query:   1854 TCTCGCTCTGTCGCCAGGCTGGAGTGTAGTGGCATGATCTCACCACACTGCAACCTCTGC 1795
              | ||||    | | || || || |||||| |||||| ||||||||        |||||||||||| |
Sbjct:  21011 TTTCGCCAGGCTGGCGTGCAGGAGTGCAGTGGCGTGATCTCAGTTCACTGCAACCTCCAC 21070

Query:   1794 CTCCCGGGTTCAAACGATTCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACTACAGGCATG 1735
              | || ||| |||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct:  21071 CACCTGGGGTCAAGTGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGCACC 21130
```

```
Query:  1734 TGCCAACACACCCAGCTAATTTTTGCACTTTCAGTAGAGATGGGGTTTCACTATGTTGGT 1675
             IIII IIIIII IIIIIIIIIIIIII I III IIIIIIIIIIIIIIIIII IIIIIIII
Sbjct: 21131 CGCCAGCACACACAGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTCACCATGTTGGT 21190

Query:  1674 CACTATGGTCTTGATCTCTTGATCTCGTGATCTACCCACCTTGGGTTCCCAAAATGTTGG 1615
             II IIIIIIII IIIIIIIII I IIIIIII IIII III II III IIII II III
Sbjct: 21191 CAGGATGGTCTCTATCTCTTGACCCCGTGATCCACCCGCCTAGGCTTCTCAAAGTGCTGG 21250

Query:  1614 GATTACAGGTGTGAGCCACTGCACCAGGCAAAC 1582
             IIIIIIIII  IIIIIII IIIII II II
Sbjct: 21251 GATTACAGGCAAGAGCCACCGCACCCAGCCCAC 21283
```

 Score = 878 (242.6 bits), Expect = 1.5e-62, P = 1.5e-62
 Identities = 218/271 (80%), Positives = 218/271 (80%), Strand = Minus

```
Query:  1856 AGTCTCGCTCTGTCGCCAGGCTGGAGTGTAGTGGCATGATCTCACCACACTGCAACCTCT 1797
             IIIIII IIIIIIIIIIIIIIIIIIIIII IIIIIIIII IIIII I  IIIIIIIIIII
Sbjct: 35428 AGTCTCACTCTGTCGCCAGGCTGGAGTGCAGTGGCATGGTCTCAGCTAACTGCAACCTCC 35487

Query:  1796 GCCTCCCGGGTTCAAACGATTCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACTACAGGCA 1737
             III III IIIIIIII IIIIIIIIIII IIIIIIII  IIIIIIIIIII IIIIII
Sbjct: 35488 GCCACCCAGGTTCAACTGATTCTCCTGCTTCAGCCTCCTGAGTAGCTGGGATTACAGGTG 35547

Query:  1736 TGTGCCAACACACCCAGCTAATTTTTGCACTTTCAGTAGAGATGGGGTTTCACTATGTTG 1677
             I IIIII II  III IIIIIIIIIII I IIII IIIIII  IIIIIIIIII II II
Sbjct: 35548 CGCGCCACCATGCCCGGCTAATTTTTGTATTTTCTGTAGAGGCAGGGTTTCACCATCTTT 35607

Query:  1676 GTCACTATGGTCTTGATCTCTTGATCTCGTGATCTACCCACCTTGGGTTCCCAAAATGTT 1617
             IIII    IIIIII II I I III III IIIIIIIIII III II  III III I I
Sbjct: 35608 GTCAGGCTGGTCTCGAACACCTGACCTCATGATCTACCCGCCTCGGCCTCCTAAAGTTCT 35667

Query:  1616 GGGATTACAGGTGTGAGCCACTGCACCAGGC 1586
             IIIIIIIIIII IIIIIIIIIII II III
Sbjct: 35668 GGGATTACAGGCGTGAGCCACTGCGCCCGGC 35698
```

 Score = 731 (202.0 bits), Expect = 2.9e-104, Poisson P(2) = 2.9e-104
 Identities = 191/247 (77%), Positives = 191/247 (77%), Strand = Minus

```
Query:  1863 GAAACCAAGTCTCGCTCTGTCGCCAGGCTGGAGTGTAGTGGCATGATCTCACCACACTGC 1804
             II II IIIIII I         IIIIIII IIIII IIIIIII  IIIII I IIIIII
Sbjct: 24275 GAGACAGAGTCTTGTCTGTCACCCAGGCTTGAGTGCAGTGGCACAATCTCGGCTCACTGC 24334

Query:  1803 AACCTCTGCCTCCCGGGTTCAAACGATTCTCCTGCCTCAGCCTCTCAAGTAGCTGGGACT 1744
             IIIII I IIIIII I II II IIIIIIIII IIIIIIIIII I III IIIIII I
Sbjct: 24335 AACCTTGGTCTCCCAGATTAAAGCGATTCTCCTCCCTCAGCCTCCCGAGTCACTGGGATT 24394

Query:  1743 ACAGGCATGTGCCAACACACCCAGCTAATTTTTGCACTTTCAGTAGAGATGGGGTTTCAC 1684
             IIIII II IIIIII III IIIIIIIIIIIIIIII I III IIIIIII IIIIIIIIII
Sbjct: 24395 ACAGGTATATGCCACCACGCCCAGCTAATTTTTTTATTTTTAGTAGAGGTGGGGTTTCAC 24454
```

7

HGS

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Query:  1683 TATGTTGGTCACTATGGTCTTGATCTCTTGATCTCGTGATCTACCCACCTTGGGTTCCCA 1624
             ||| ||||| || | ||||||| || ||| ||| |||||||||  ||||||| ||  |||||
Sbjct: 24455 TATATTGCCCAGTCTGGTCTCGAACTCCTGACCTCGTGATCCGCCCACCTCGGCCTCCCA 24514


Query:  1623 AAATGTT 1617
             || || |
Sbjct: 24515 AAGTCCT 24521
```

Protein BLAST Analysis

Protein Blast of HTPAN08 Full Contig + Screen

Query= HTPAN08XX   HGS#285507
       (1863 letters)

Translating both strands of query sequence in all 6 reading frames

Database: nr
           113,553 sequences; 31,868,292 total letters.
Searching..done

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Smallest Poisson Probability P(N)	N
pir|S|A40201	artifact-warning sequence (trans...	+3	241	1.4e-76	3
pir|S|C40201	artifact-warning sequence (trans...	+2	246	7.9e-59	2
pir|S|F40201	artifact-warning sequence (trans...	+3	180	1.1e-20	2
gp|X55777|HSMHCHHS_2	H.sapiens Mahlavu hepatocellular...	+3	190	1.9e-19	1
pir|S|D40201	artifact-warning sequence (trans...	+3	81	2.3e-18	4
gp|L27065|HUMNF2A_1	NF2 gene product [Homo sapiens]	-3	139	7.4e-14	1
gp|L20321|HUMSTK2A_1	protein serine/threonine kinase ...	-1	137	3.0e-12	1
pir|S|E40201	artifact-warning sequence (trans...	+2	98	1.0e-11	3
gp|S58722|S58722_1	X-linked retinopathy protein (3'...	-1	128	1.5e-11	1
pir|S|A46010	X-linked retinopathy protein (C-...	-1	128	1.5e-11	1
gp|M84237|HUMIGTB1A_2	integrin beta-1 subunit [Homo sa...	-3	116	1.9e-10	1
pir|S|A42442	beta 1 integrin subunit, beta 1S...	-3	116	1.9e-10	1
gp|L24521|HUMTRRP_1	transformation-related protein [...	-3	120	1.9e-09	1
gp|K02113|CHKVTTB_1	Chicken vitellogenin gene coding...	+3	72	1.0e-07	2

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Project Worksheet
fas ligand

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HGS

gp|L11672|HUMKRUPZN_1	zinc finger protein [Homo sapiens]	+1	108	1.9e-07	1
gp|X13607|GGVITIIG_1	vitellogenin [Gallus domesticus]...	+3	72	1.1e-06	2
gp|M18060|CHKVITC_1	Chicken vitellogenin gene, compl...	+3	72	1.1e-06	2
gp|U03470|RNU03470_1	ligand for Fas antigen [Rattus n...	+3	84	1.8e-06	2

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 84 (40.9 bits), Expect = 0.0019, P = 0.0019
Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +3

Query: 750 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 851
              G + +S +   + G LVI+E G Y++YS+ YFR Q
Sbjct: 164 GTALISGVKYKKGGLVINEAGLYFVYSKVYFRQQ 197

Score = 66 (32.2 bits), Expect = 1.8e-06, Poisson P(2) = 1.8e-06
Identities = 12/39 (30%), Positives = 22/39 (56%), Frame = +3

Query: 990 YSIYQGGIFELKENDRILVSVINEHLIDMDHEASFFGAF 1106
              +S Y G +F L   D + V+++   LI+ +   +FFG +
Sbjct: 238 HSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFGLY 276

Full Length Information

Full length sequence of HTPAN08XX HGS# 285507

GGCACGAGCACATTGTCTTCTCCAAACTCCAAGAATGAAAACGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTG
GGCATTCATTCCTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTTACTACATCTATTCCCAAAC
ATACTTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATATTTACAAATACACAAGTTAT
CCTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAG
GGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTGTGGTTTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCA
GTTTTTTTCGGGGCCTTTTTAGTTGCCTAACTGACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTCAGTTTTCAGGATGA
TACACTATGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAACCCTCTATGCAATCTGAGTA
GAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTGAAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGAT
CTTTCAGGACTCTACCTCATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATTAATGCAATGGTTACATCT
TCTGGCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAACGCAACAATCCATCTCTCAAGTAGTGTATCACAGTAGTAGCC
TCCAGGTTTCCTTAAGGGACAACATCCTTAAGTCAAAAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGG
CTCACACCTGTAATCCCAACATTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGATCAAGACCATAGTGACCAACATAG
TGAAACCCCATCTCTACTGAAAGTGCAAAAATTAGCCTGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAGAGGCTGAGG
CAGGAGAATCGTTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACACTCCAGCCTGGCGACAGAGCGAGA
CTTGGTTTCAAAAAAAAAAA

Human Genome Sciences, Inc.
Matched Sequence Worksheet
HTPAN08R   : tumor necrosis factor (TNF-alpha)

Search Results

Description	Score	Overlap	Start	End	% Sim	% Iden	LEnd	REnd	Date	Meth
Tumor necrosis factor precursor - Human	20	PIR:A44189	104	143	57.50	35.00	59	178	08/24/93	zest
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CAC	20	SP:P01375	104	143	57.50	35.00	59	178	08/24/93	zest

Sequence

tumor necrosis factor (TNF-alpha)
HTPAN08R   Length: 230 Sunday 20, 1993 13:50 Check: 9601 ..

```
  1 CACATTGTCT TCTCCAAACT CCAGAATGA AAAGCCCTG GGGCGCAAA
 51 TAAACTCCTG GGAATCATCA AGGAGTGGGC ATTGATTCCT GAGCAACTTG   46-5
101 CACTTGAGGA ATGGGTGAACT GGTCATCCAT GAAAAGGGT TTTACTTACAT
151 CCATTCCCAA ACATACTTTG GATTTCAGGA CGAAATAAAA GAAAACACAA   1573
201 AGAACGACAA AGAAATGGTC CAAATATTTT
```

ii

HGS Sequencing Worksheet

INVESTIGATOR: AK, Ho, Suk, LC, DB   DATE: 9/1

LIBRARY/METHOD: Misc DP/DT?   PLATE #: _____

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments	
1	HTPBC24Ra	AK boiling	DP	Reverse		NS	N
2	HTPBC24Rb					weak	R
3	HIBCW23Ra						320
4	HIBCW23Rb					NS-weak	&NS
5	HTPAN08Ra					miss-C	*
6	HTPAN08Rb	↓	↓			miss-C	R
7	HIBCK00R	Ho Magic Mini				weak	M
8	HPMAM00R	↓ ↓					282
9	HTEAH87R	Suk Midi					391
10	HPLEB38R					weak	NS
11	HIBEH64R	↓ ↓				weak	37 369
12	PGEM( )R	control			↓		370
13	HTPBC24Fa	AK boiling		Forward		NS-weak	ND
14	HTPBC24Fb						350
15	HIBCW23Fa						344
16	HIBCW23Fb					NS-weak	NDF
17	HTPAN08Fa						320
18	HTPAN08Fb	↓ ↓					405
19	HTEAH87F	Suk Midi				weak	M
20	HPLEB38F	↓ ↓					276
21	HIBEH64F	↓ ↓					477
22	HIBCK00F	Ho Magic Mini					426
23	HPMAM00F	↓ ↓ ↓				weak poly T, DK	
24	HASSB35F	LC	↓	↓		weak poly T	R
25	PGEM( )DT	control	DT				*
26	HIBCK0000694	Ho		692		weak-US	N
27	HPMAM0000693	↓		653		weak-US	M
28	HFKBE9500647	DB boiling		647			340
29	HIBEI0200646	↓ ↓		646		weak-US	341
30	HASSB3500001	LC		VDRF1			293
31	HASSB3500187	↓		G187			R
32							
33							
34							
35							
36							

.dditional Comments:

Date of Run: 9-10-73

Catalyst #: 8-10-93 Manual RYS/KHC

Sequencer #: 09

Results Folder: 9-(-3 DNA09

Blast Analysis: _____

Renee 13

HGS Sequencing Worksheet

INVESTIGATOR: AK, Ho; Suk, LC. DB   DATE: 9/1

LIBRARY/METHOD: Misc DP/DT1   PLATE #: _____

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments	
1	HTPBC 24Ra	AK boiling	DP	Reverse		NS	N
2	HTPBC 24Rb					weak	R
3	HIBCW 23Ra						320
4	HIBCW 23Rb					NS-weak	ENS
5	HTPAN 08Ra					miss-C	*
6	HTPAN 08Rb	↓	↓			miss-C	R
7	HIBCK00R	Ho Magic Mini				weak	M
8	HPMAM00R	↓	↓				282
9	HTEAH87R	Suk Midi					391
10	HPLEB38R					weak	NS
11	HIBEH64R	↓	↓			wash	37 36S
12	PGEM( )R	control			↓		370
13	HTPBC24Fa	AK boiling		Forward		NS-weak	ND
14	HTPBC24Fb						350
15	HIBCW23Fa						344
16	HIBCW23Fb					NS-weak	NDF
17	HTPAN08Fa						320
18	HTPAN08Fb	↓	↓				4/5
19	HTEAH87F	Suk Midi				weak	M
20	HPLEB38F						276
21	HIBEH64F	↓	↓				477
22	HIBCK00F	Ho Magic Mini					426
23	HPMAM00F	↓	↓	↓		weak poly T DP	
24	HASSB35F	LC			↓	weak poly T	R
25	PGEM( )DT	control	DT				*
26	HIBCK000694	Ho		692		weak-NS	N
27	HPMAM000693	↓		693		weak-NS	M
28	HFKGE9500647	DB boiling		647			340
29	HIBEI0200646	↓ ↓		646		weak-NS	340
30	HASSB35000	LC;		VDRF1			293
31	HASSB35000187	↓		G187			R
32							
33							
34							
35							
36							

Additional Comments:

Date of Run: 9-10-73

Catalyst #: 9-10-73 Manual RYS/HHc

Sequencer #: 09

Results Folder: 9/1→3 baAO9

Blast Analysis: _____

Renee

13

HGS Sequencing Worksheet

INVESTIGATOR: JG, GLY, JW, AMK
LIBRARY/METHOD:

DATE: 9/14/03
PLATE #:

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments
1 ·	HTFCU19Fa	JG. boiling	DP	Forward		T
2 ·	HTFCU19Fb					MIT
3 ·	HE8BB07Fa					
4 ·	HE8BB07Fb	↓ ↓				weak
5 ·	HLHAC23Fb	GLY; boiling				
6 ·	HFCAW19Fb	↓				N weak
7 ·	ZFBR307F	JW Magic mini				N weak
8 ·	PGEM(w23)F	control				
9 · sq	HTFCU19Ra	JG. boiling		Reverse		
10 ·	HTFCU19Rb					
11 ·	HE8BB07Ra					
12 ·	HE8BB07Rb	↓ ↓				
13 ·	HPLiB74Rb	GLY boiling				
14 ·	HPRAA08Rb	magic				weak
15 ·	HPLB227Rb					weak
16 ·	HPMAK36Rw					weak
17 ·	KPMAK36Rb	↓ ↓				weak
18 ·	ZFBR307R	JW Magic Mini				weak R
repeat 19 ·	HTPAN08Ra	AMK				
repeat 20 ·	HTPAN08Rb	↓				
21 ·	PGEM(w35)R	Control	↓	↓		
22						
23						
24						
25						
26						
27						
28						
29						
30						
31						
32						
33						
34						
35						
36						

Rev. LOT A3i/cce / Forward M3ECo8

Additional Comments:
Date of Run: 9/14/93
Catalyst #: Biomek

Sequencer #: 05
mix + KAC Results Folder: 09/15/93 DNA 05 KAG

Blast Analysis:

Run G   14

HGS Sequen‚ ng Worksheet

INVESTIGATOR: JG, GLY, JW, AMK

LIBRARY/METHOD:

DATE: 9/14/93

PLATE #:

Sample No.	Sample Name	Sample Preparation Comments	Chemistry Dye Prim/ Dye Term	Primer Name	Sequence Protocol	Sequence Comments
1	HHFCU19Fa	JG, boling	DP	Forward		
2	HHFCU19Fb					T
3	HE8BB07Fa					HIT
4	HE8BB07Fb	↓ ↓				weak
5	HLHAC23Fb	GLY, boily				
6	HFCAW19Fb	↓				N weak
7	ZFBR307-F	JW Magic mini				N weak
8	PGEM(···)F	↑prep		↓		
9	HHFCU19Ra	JG boily		Reverse		
10	HHFCU19Rb	↓				
11	HE8BB07Ra					
12	HE8BB07Rb	↓ ↓				
13	HPLiB74Rb	GLY boily				
14	HPRAA08Rb	↓ magic				weak
15	HPLBQ27Rb					weak
16	HPMAK36Rw					weak :)
17	XPMAK36Rb	↓ ↓				weak
18	ZFBR307-R	JW Magic Mini				weak R
19	HTPAND8Ra	AMK				
20	HTPAND8Rb	↓				
21	PGEM(·3S)R	Control	↓	↓		
22						
23						
24						
25						
26						
27						
28						
29						
30						
31						
32						
33						
34						
35						
36						

repeat 19
repeat 20

Additional Comments:

Date of Run: 9/14/93 Sequencer #: 05

Catalyst #: Biomek minys + KAG Results Folder: 09/15/93 DNA OS KAG

Blast Analysis: _____

HHFCU19G   101,66,42,23 85 12.32   Trash T   17 Poly T at 55
HHFCU19Fb   93.9466 38 85 12.94   Trash M/T   Poly T at 53; appears mixed
HE8BB07Fa   114,55,42,43 85 -12.00   72→310   ~ 124/310-72
HE8B207Fb   67,78,43,27 43 -17.00   80→300   144/300-30
HLHAC23Fb   29,71,50,43 33 11.76   105→290   34/290-05
HFCAW19Fb   no analyzed data   N
ZFBR307F   no analyzed data   N
PGEM025F   112,119,45,53 85 -12.00   104→285   7N/285-104
HHFCU19Ra   123,95,73,60 35 12.51   106→470¹   2N/470-106
HHFCU19Rb   112,82,55,59 85 12.95   103→48c¹   2N/48c-163
HE8BB07Ra   172,15,29,69 85 12.95   104→476¹   1N/28¹-c9
HE8B307Rb   246,137,105,87 85 12.37   68→476¹   2N/476-68
HPLYB34Rb   109,90,62,52 63 12.51   104→460¹   6N/46c-104
HPRAA08Rb   70,54,38,37 51 13.36   87→42c¹   1cN/42c-57
HPLBG27Rb   72,45,37,34 45 13.48   65→370¹   7N/370-55
HPMAK362w   no analyzed data   N
HPMAK362b   74,53,42,33 85 13.03   87→430¹   1cN/430-37
ZFBR307R   44,35,36,26 35 -12.00   Trash R
HTPANO3Rg   155,115,86,95 85 12.82   105→428   6N/428-05
HTPAN08Rb   107,78,60,50 85 12.13   52→420¹   7N/42c-52
PGEM038R   92,55,44,35 85 13.25   37→310   114N/310-37

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Human Genome Sciences, Inc.
Matched Sequence Worksheet
HTPAN08R   : tumor necrosis factor (TNF-alpha)

Search Results

Description	Score	Overlap	Start	End	% Sim	% Iden	LEnd	REnd	Date	Meth
Tumor necrosis factor precursor - human	20	PIR:A44189	104	143	57.50	35.00	59	178	08/24/93	zest
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CAC	20	SP:P01375	104	143	57.50	35.00	59	178	08/24/93	zest

Sequence

tumor necrosis factor (TNF-alpha)

HTPAN08R   Length: 230 Sunday 20, 1993 13:50 Check: 9601 ..

```
  1 CACATTGTCT TCTCCAAACT CCAAGAATGA AAAGGCTCTG GGCGCAAAA
 51 TAAACTCCTG GGAATCATCA AGGAGTGGGC ATTGATTCCT GAGCAACTTG     46-S
101 CACTTGAGGA ATGGTGAACT GGTCATCCAT GAAAAAGGGT TTTACTACAT
151 CTATTCCTAA ACATACTTTC GATTTCAGGA GGAAATAAAA GAAAACACAA     1575
201 AGAACGCACAA ACAAATGGTC CAATATATTT
```

Applied Biosystems

Synthesis Order - htpan08 157-s

Run date: 9/20/93
Run ID: 685 AMK
Customer: amk   *Zlemer*

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: htpan08 157-s
Sequence: CCA AAC ATA CTT TCG ATT TCA GGA GG

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

PO1

Comments: 1:250 Dilution

$OD_{260} = 0.1479$

$OD_{280} = 0.0885$ ✓

$OD_{260}/280 = 1.6688$

$0.1479 \times 250 \times 33 = 1.22 \, ug/ul.$

$(26)(330) = 8580$

$(1.22 ug/ul)/8580) \times 10^6 = 142.2 \, pmol/ul$

Redo's
Human Genome Sciences, Inc.

Plate I.D. **Misc. DT/pP**

Date Initiated: **9/23/93**

Results Folder: **09/25/93 05**

Date Completed: **9/26/93**

% Good: **16/27**

	Templates	Sequence Reaction	Gel Run
Method:	Misc	Method: Manual	Machine ID: 05
Prep Person:	Gly, Jw, Sm, Amk, DB, YFW	Prep Person: Ming	Gel Loader: ming
Prep Date:	9/22/93	Prep Date: 9/24	Run Date: 9/24

#	Sample Name	Chemistry DP/DT	Primer Name	Signal Strength C	A	G	T	Rate Spacing	Vector	Edited Length	Ns!	Trash Code
1	PGEMD Test 1	DT	M13-21	255	169	160	82	9.71		350	1	
2	SODI9 A00474a		474	−	−	−	−	~	−	−	−	N
3	B00474a			−	−	−	−	−	−	−	−	N
4	C00474a			31	33	30	39	−12				R
5	D00474a			35	37	28	35	−12				R
6	E00474a			120	75	71	41	9.78				R
7	F00474a			−	−	−	−	−	−	−	−	N
8	G00474a			86	62	47	49	~12				R
9	H00474a			−	−	−	−	−	−	−	−	N
10	ZFBR21190232		232	48	50	34	40	9.89	−	350	9	
11	HIBEC6900680		680-S	558	438	288	210	9.90		530	6	
12	HE8AY2900202		202-S	29	32	29	32	9.69	−	−	−	R
13	HTPANA800157		157-S	404	762	381	122	9.92		350	6	
14	HHPBF7300001		P1	584	464	625	191	9.93		450	6	
15	HE8AE4500002		P2	40	32	25	26	9.79	−	−	−	R
16	HE8AE4500004		P4	132	206	192	49	9.93		470	8	
17	HHPBF7300508		P508	396	530	608	102	9.89		410	3	
18	HHPBF7300509		P.509	337	480	424	117	9.88		520	4	
19	HLFCD4400689	✓	689	−	−	−	·	−	−	−	−	N
20	PGEM & 38P	DP	Rev	338	252	197	172	10.06		460	5	
21	HCAAA02Ra			364	275	170	119	10.11		460	10	
22	HTYSE16Ra			89	199	110	97	10.01		530	5	
23	HE7SE81Rc	✓	✓	270	192	114	81	10.03		610	8	
24	HCAAA02Fa	DP	FOR	409	288	154	56	9.97		480	5	
25	HE7SE81Fa			544	335	203	118	10.01		570	9	
26	HTYSE16Fa			116	72	36	28	9.91		390	2	
27	PGEME 37F	✓	✓	320	82	132	83	9.95		500	10	
28												
29												
30												
31												
32												

~60 < poly

Analyzed by: **ASP**

Factura/Blast Analysis: _____

Additional Comments: **RE - TRACTED**

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Human Genome Sciences, Inc.

Plate I.D. __Misc DP__

Date Initiated: __9/23/93__

Date Completed: __9/25/93__

Results Folder: __09/25/93 DNA 11__

% Good: __18/30__

	Templates		Sequence Reaction		Gel Run
Method:	Misc	Method:	Manual	Machine ID:	11
Prep Person:	AMK, JW	Prep Person:	Debbie	Gel Loader:	Debbie
Prep Date:	9/25/93	Prep Date:	9/24	Run Date:	9/24

#	Sample Name	Chemistry PRDT	Primer Names	C	A	G	T	Bases Spacing	Vector	Edited Length	Seq Ns	Track Code
1	PGEM F 451-027 1-32f(+)	DP	FOR							440	1	-
AMK 2	DNase P F											N
3	HIBEC69F									540	22	
4	HIBCW23F									300		T
5	HE8AY29F									300		T
6	HTPAN08F									350		T
JW 7	HFLBM01F											R
8	02F									360		
9	03F											T
10	04F											T
11	05F											R
12	06F											T
13	07F											R
14	08F											A,R
15	09F											T
AMK 16	DNase P R		REV									R
17	HIBEC69R									400	2	
18	HIBCW23R									500	2	
19	HE8AY29R									370		
20	HTPAN08R									290	32	M
JW 21	HFLBM01R									30	2	
22	02R									350	5	
23	03R									320	2	
24	04R									260	12	
25	05R									370	20	
26	06R									150	4	
27	07R											R
28	08R											R
29	09R									260	15	
30	PGEM R 451-032 1-32f(+)									385	10	
31												
32												

Analyzed by: _____

Factura/Blast Analysis: _____

Additional Comments:

20

Applied Biosystems

Synthesis Order - 5426 HTPAN08r - 66s

Run date: 2/3/94
Run ID: 5426 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5426 HTPAN08r - 66s
Sequence: CAT CAA GGA GTG GGC ATT C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

POS

Comments:

RPS

21

ab *Applied Biosystems*

Synthesis Order - 5424

Run date: 2/3/94
Run ID: 5424 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5424 HTPAN08F - 318s
Sequence: GGT GCC TCT TCT CTC TTT TG

Cycle: 40' nM CE

End procedure: End CESS
DMT: Off

P03

Comments:

 Sent to "Synthesizer-2" col 2 seq 32 at 2/3/94 2:57 PM.

Applied Biosystems

Synthesis Order - 5425 HTPAN08R - 404s

Run date: 2/3/94
Run ID: 5425 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5425 HTPAN08R - 404s
Sequence: GAG CAC TTG ATA GAC CAT G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

P04

Comments:

Plate I.D. **misc DT**

Date Initiated: **2/8/94**

Date Completed:

Results Folder: **HGS 47 2/9/94**

% Good: **DT80 11/20**

Templates	Sequence Reaction	Gel Run
Method:	Method: **Manual**	Machine ID: **47**
Prep Person:	Prep Person: **JMA**	Gel Loader: **JMA**
Prep Date:	Prep Date: **2/8/94**	Run Date: **2/8/94**

#	Sample Name	Chemistry DP/DT s	Primer Name	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1		DT										
2	PGEM DT			A8	263	421	156	10.59	5	465	4N	
3	PD10HCT 7311 SDS			26	83	103	42	11.02	10	340	8N	
4	PD10HCT 7312 SDS											N
5	PD10HCT 7313 SDS			17	46	52	23	11.20	10	290	8N	
6	PD10HCT 7314 SDS											N
7	HJB4VGC P589			45	109	131	58	10.84	40	360	3N	
8	HJB4VGC P5317			36	158	133	44	10.57	40	420	13N	
9	HIBEJ 89536 FP03											N
10	HIBEJ 895 36 RP03											N
11	HIBEJ 895 36 RP2											N
12	HIBEJ 895 36 RP1											N
13	HIBEJ 895 36 FP											N
14	HIBEJ 895R P11											N
15	HIBEJ 895 P11											N
16	HIBEJ 895 RP21											N
17	HIBEJ 895 RP03			48	54	57	48	10.92	40	380	5N	
18	HIBEJ 895 FP035			44	44	45	47	10.51	90			L
19	HIBEJ 895 FP031											N
20	HIBEC 695 FP011											N
21	HIBEC 695 RP011											N
22	HIBEC 695 FP031			81	71	34	75	-12				RC
23	HTIS042RP1b			47	208	316	130	-12				RC
24	HIBEH649RP01											N
25	HIBEH64RP02			70	100	163	48	10.76	40	400	3N	
26	HIBEH64RP03			91	72	131	37	10.95	50	280	22N	
27	HTPAN08 RP03			147	50	161	135	10.35	30	270	3N	
28	HTPAN08 RP04											N
29	HTPAN08 RP05			194	257	446	337	10.53	10	390	12N	
30	HE7SE29RP01			36	65	42	52	10.51				m
31	HPRAL89 RP01b			48	170	254	121	10.71	40	400	5N	
32												

Analyzed by: ~~~

Factura/Blast Analysis:

Additional Comments: { samples in brackets - not enough for a seq. redo
- please resubmit

24

Human Genom. Sciences, Inc.

Plate I.D. _mwc dt's #2_

Date Initiated: _2/12/94_

Date Completed: _2/13/94_

Results Folder: _HGS 472.139_

% Good: _18132   56%_

Templates	Sequence Reaction	Gel Run
Method: _Mu._	Method: _Manual_	Machine ID: _47_
Prep Person:	Prep Person: _DMD_	Gel Loader: _DMD_
Prep Date:	Prep Date: _2.13.94_	Run Date: _2.13.94_

#	Sample Name	Chemistry DP/DT	Primer Name	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	HGEN1 DT	DT		461	309	128	153	10.07	≈20	350	2N	
2	HEUBG 49 RPC1		RPC1									N
3	HSBAT 60b RPC1		1431	417	259	167	150	10.60	≈20	390	1N	
4	" & RPC1		1431	365	233	165	138	10.02	≈20	400	3N	
5	HFTAO 67 NP20		5454									N
6	HLTAW 73 RP11		5445	155	125	77	38	10.06	≈30		7N	
7	" FP7		5479									N
8	H PRTR 45 RPC1		5470	525	308	174	131	10.16	≈20	420	2N	
9	" b RP02		5471	428	273	166	177	10.12	≈40	410	0N	
10	HLTAW 73 P13		5483	120	55	42	24	10.08	≈30	270	8N	
11	HETAO 67 RP106		5465	122	82	44	31	10.13				many N's
12	" CP06b		5461	101	79	51	35	10.16	≈40	310	11N	
13	" FP01		5370	148	86	54	50	10.23	≈20	290	5N	
14	" FP11b		5473	109	76	45	43	10.14				many N's
15	HLTAW 73 RP3b		5366	30	42	58	25	-12				R
16	HLTAW 73 FP15		5360									N
17	HETAO 47 FP01		5472	153	175	154	104	-12				R
18	HTPANT9 R P03a		3195	478	389	365	95	10.02	≈30	290	0N	
19	" RPC4c		4545									N
20	" RPC5c		665	269	464	161	73	10.21	≈40	300	6N	
21	HETSE 29 RP012		5465									N
22	HPRAL 47 RPC1c		2235	240	145	78	62	10.17	≈50	330	1N	
23	HETPA 3 FP12		5472	243	172	110	85	10.08	≈20	250	6N	
24	" FP13		5473	466	310	225	159	10.17	≈40	300	1N	
25	" FPC4		5474	634	269	172	128	10.23	≈50	310	2N	
26	" FP15		FP15	415	195	116	103	10.14	≈50	330	4N	
27	" RPC4		RPC4	434	309	165	173	10.39	≈30	220-A	2N	*
28	" RPC5		RPC5	177	158	76	69	10.29	≈50	300	3N	
29	HLFBE 105 GL RP1C		5415	59	48	26	20	10.26				many N's
30	RP1Ca		5415	69	50	27	20	10.34				many N's
31	HLFBE 105 GL RP11		5411									N
32	RP11c	DT	5411									N

Analyzed by: _ASP_

Factura/Blast Analysis: _____

Additional Comments: *#27 → 250 bases then poly A's

uploaded Scientist + Full length

25

Applied Biosystems

Synthesis Order - 5688 HTPAN08F 488-AP07

Run date: 3/3/94
Run ID: 5688
Customer: A KIM

1.   CX
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: HTPAN08F 488-AP07
Sequence: CTG CTA GCA AAC TGA TAT GAG

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-2" col 4 seq 34 at 3/8/94 2:07 PM.

26

Synthesis Order - 5676 HTPAN08 333-SP06

Run date: 3/3/94
Run ID: 5676 AK
Customer: A KIM

1.   JPW
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 5676 HTPAN08   333-SP06
Sequence: GGG GGA ATA TTT GAG CTT AAG G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
  Sent to "Synthesizer-1" col 2 seq 32 at 3/7/94 8:27 AM.

27

Human Genome Sciences, Inc.   Plate I.D.(s) __DP'S REV_____ _____

Date Initiated: 3/10/94 _____   Results Folder: HGS 50 3/11/94

Date Completed: 3/11/94 3/11/94   % Good: 21/25   % Good: _____

Templates	Sequence Reaction	Gel Run
Method: ————	Method: MANUAL/BIOMEK	Machine ID: 50
Prep Person: MISC	Prep Person: BCI	Gel Loader: TAL
Prep Date: ————	Prep Date: 3/10/94	Run Date: 3/10/94

#	Sample Name	Scientist name/init control	Primer DP/DT DP R	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEMR			374	254	55	99	9.92	85	200	1	
2	HHPEB36R	HLI		245	161	96	50	9.97	96	234	12	
3	HOSAA70R	HLI		173	115	63	61	10.09	105	295	3	
4	HPBEC27R	HLI		188	135	59	57	9.51	101	300	9	
5	HLTAI45R	HLI		254	195	81	60	10.02	93	307	4	
6	HE9DR66R	HLI		92	81	41	45	9.56	90			R
7	HMPTE39R	HLI		214	132	55	53	10.05	100	230	2	
8	HLTBX37R	T. Curtis										N
9	HTPANO8S01R	ANN KIM		125	135	47	39	10.21	110	260	4	
10	HTPANO8S02R	ANN KIM		191	131	59	59	9.93	104	226	3	
11	HTPANO8S03R	ANN KIM		57	102	45	40	9.88	103			m
12	HTPANO8S04R	ANN KIM		216	170	65	60	10.08	105	275	3	
13	HTPANO8S05R	ANN KIM		331	270	83	87	9.97	98	272	2	
14	HTPANO8S06R	ANN KIM		209	222	80	71	9.54	95	235	4	
15	HTPANO8S07R	ANN KIM		116	72	37	33	9.52	105	215	4	
16	HTPANO8S08R	ANN KIM		150	102	46	42	9.94	109	212	7	
17	HTPANO8S09R	ANN KIM		102	102	43	34	10.00	165	245	4	
18	HTPANO8S10R	ANN KIM										N
19	HTPANO8S11R	ANN KIM		237	197	74	73	10.13	99	255	3	
20	HTPANO8S12R	ANN KIM		214	159	57	52	9.99	102	268	1	
21	HTPANO8S13R	ANN KIM		140	128	75	58	10.03	90			R
22	HTPANO8S14R	ANN KIM		269	179	75	61	9.98	99	271	4	
23	HSABH13S05R	ANN KIM		130	116	31	37	10.09	105	295	4	
24	HETDE26R	SUK		209	106	70	58	10.02	99	230	2	
25	HFGAN12R	SUK										N
26	HATBG78R	SUK		201	229	97	104	10.09	94	300	2	
27	HHPI84R	SUK		247	154	99	131	10.13	92	298	6	
28	HHPEC49S3RA	SUK										N
29												
30												
31												
32												

Analyzed by: JMD   Factura/Blast Analysis: _____

Uploaded by: ✓   Folder: Full length + scientist

Additional Comments:

28

Human Genome Sciences, Inc.

Plate I.D.(s) __DT's #2__

Date Initiated: __3/8/94__
Date Completed: __3/9/94__

Results Folder: __HGS 43 3/9/94__

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: __43__
Prep Person:	Prep Person: __CDL__	Gel Loader: __BCI__
Prep Date:	Prep Date: 03/08/94	Run Date: __3/8/94__

#	Sample Name	Scientist name/init control	Primer DP/DT DT	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% N	Trash Code
1	PGEDMDT											N
2	HIBEC69S07RP04	ANN KIM	672	—								N
3	HIBEC69S08RP04	ANN KIM	672	29	25	8	69	72.00				L
4	HIBEC69S09RP04	ANN KIM	672	—								N
5	HIBEC69S10RP04	ANN KIM	672	—								N
6	HIBEC69S11RP04	ANN KIM	672	—								N
7	HIBEC69S12RP04	ANN KIM	672	—								N
8	HIBEC69S13RP04	ANN KIM	672	—								N
9	HIBEC69S14RP04	ANN KIM	672									N
10	HIBEC69S15RP04	ANN KIM	672	—								N
11	HIBEC69S16RP04	ANN KIM	672	—								N
12	HIBEC69S17RP04	ANN KIM	672	—								N
13	HIBEC69S18RP04	ANN KIM	672	244	159	160	75	10.77	20	330	3	
14	HIBEC69RP04	ANN KIM	672	—								N
15	HTPAN08S01RP03	ANN KIM	5424	—								N
16	HTPAN08S02RP03	ANN KIM	5424	—								N
17	HTPAN08S03RP03	ANN KIM	5424	38	111	139	111	10.87	10	500	3	
18	HTPAN08S04RP03	ANN KIM	5424	106	313	356	350	10.94	10	550	2	
19	HTPAN08S05RP03	ANN KIM	5424	—								N
20	HTPAN08S06RP03	ANN KIM	5424	365	441	181	595	-12.00				R / SFS3
21	HTPAN08S07RP03	ANN KIM	5424	—								N
22	HTPAN08S08RP03	ANN KIM	5424	—								N
23	HTPAN08S09RP03	ANN KIM	5424	—								N
24	HTPAN08S10RP03	ANN KIM	5424	—								N
25	HTPAN08S11RP03	ANN KIM	5424	—								N
26	HTPAN08S12RP03	ANN KIM	5424	—								N
27	HTPAN08S13RP03	ANN KIM	5424	41	139	155	129	10.86	10	420	4	
28	HTPAN08S14RP03	ANN KIM	5424	212	258	212	248	10.69	10	400	3	
29	HTPAN08RP03	ANN KIM	5424	—								N
30	HRGBF22RP01	BEDNARI	5618	—								N
31	HHPEC49S13RP12	SUK		—								N
32	HHPEC49S13FP12	SUK		—								N

Retracted Serial

Analyzed by: __Serial__   Factura/Blast Analysis: _____

Uploaded by: ____   Folder: __full length / Scientists__

all samples being redone in Seg.

29

— REDOING GEL FROM 31494

Human Genome Sciences, Inc.

Plate I.D.(s) _DT'S #2_

Date Initiated: _3/8/94 Redos_   Results Folder: _43 HGS 3/10/94_

Date Completed: _____   % Good: _3/24_   % Good: _2-/7_

	Templates	Sequence Reaction	Gel Run
Method:		Method: MANUAL	Machine ID: 43
Prep Person:		Prep Person: CDL	Gel Loader: BCI
Prep Date:		Prep Date: 03/08/94	Run Date: 31894

#	Sample Name	Scientist name/init control	Primer DP/DT DT	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEDMDT			2H	113	110	1H	10.45	50	450	21	
2	HIBEC69S07RP04a	ANN KIM	672	—								N
3	HIBEC69S08RP04a	ANN KIM	672	—								N
4	HIBEC69S09RP04a	ANN KIM	672	8	13	52	23	-12.00	—			R
5	HIBEC69S10RP04a	ANN KIM	672	6	15	34	16	10.15	—			R
6	HIBEC69S11RP04a	ANN KIM	672	7	16	36	17	10.52	—			R
7	HIBEC69S12RP04a	ANN KIM	672	—								N
8	HIBEC69S13RP04a	ANN KIM	672	—								N
9	HIBEC69S14RP04a	ANN KIM	672	—								N
10	HIBEC69S15RP04a	ANN KIM	672	—								N
11	HIBEC69S16RP04a	ANN KIM	672	—								N
12	HIBEC69S17RP04a	ANN KIM	672	—								N
13	HIBEC69S18RP04a	ANN KIM	672	—								N
14	HIBEC69RP04a	ANN KIM	672	133	123	71	263	10.16	—			H
15	HTPAN08S01RP03a	ANN KIM	5424	—								N
16	HTPAN08S02RP03a	ANN KIM	5424	—								N
17	HTPAN08S03RP03a	ANN KIM	5424	123	199	239	71	10.23	17	300	1	
18	HTPAN08S04RP03a	ANN KIM	5424	202	189	155	67	9.80	60	300	(	
19	HTPAN08S05RP03a	ANN KIM	5424	—								N
20	HTPAN08S06RP03a	ANN KIM	5424	—								N
21	HTPAN08S07RP03a	ANN KIM	5424	—								N
22	HTPAN08S08RP03a	ANN KIM	5424	—								N
23	HTPAN08S09RP03a	ANN KIM	5424	—								N
24	HTPAN08S10RP03a	ANN KIM	5424	—								N
25	HTPAN08S11RP03a	ANN KIM	5424	—								N
26	HTPAN08S12RP03a	ANN KIM	5424	—								N
27	HTPAN08S13RP03a	ANN KIM	5424	195	287	168	84	10.14	10	420	1.5	
28	HTPAN08S14RP03a	ANN KIM	5424	326	398	413	108	10.07	10	300	1	
29	HTPAN08RP03a	ANN KIM	5424	—								N
30	HRGBF22RP01a	BEDNARI	5618	—								N
31	HHPEC49S13RP12a	SUK										N
32	HHPEC49S13FP12a	SUK		—								N

Retracked: SPK

Analyzed by: _____   Factura/Blast Analysis: _____

Uploaded by: ___ Folder: _____

"Full Length thr"

"Sc. Seq."

30

Human Genome Sciences, Inc.

Plate I.D.(s) __MKC DT__

Date Initiated: _____

Date Completed: _____

Results Folder: __HGS 04 3/10/94__

% Good: __9/32__ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: Manual	Machine ID: 4
Prep Person:	Prep Person: WMC	Gel Loader: WMC
Prep Date:	Prep Date: 3.9.94	Run Date: 3/10/94

#	Sample Name	Scientist name/init control	Primer DP/DT DT	C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEM DT			172	125	83	76	10.49	20	350	.8	
2	HALSK38S16RP04	Ann Kim	5677									N
3	HALSK38S17RP04	Ann Kim	5677									N
4	HALSK38S18RP04	Ann Kim	5677									N
5	HALSK38S19RP04	Ann Kim	5677									N
6	HALSK38S20RP04	Ann Kim	5677	42	39	51	40	-12.00				R
7	HALSK38S21RP04	Ann Kim	5677									N
8	HALSK38S22RP04	Ann Kim	5677									N
9	HALSK38S23RP04	Ann Kim	5677									N
10	HALSK38S24RP04	Ann Kim	5677									N
11	HALSK38S25RP04	Ann Kim	5677									N
12	HALSK38RP04	Ann Kim	5677									N
13	HKMAAS1RPO2	Ann Kim	5678									N
14	HKMAAS1RPO1b	Ann Kim	5496									N
15	HTPANO8RPO6	Ann Kim	5676	140	376	113	76	10.40	35	335	1.5	
16	HE8AY29RP03	Ann Kim	5675	207	244	251	138	10.53	10	350	1.1	
17	HAPATPD10 P01	Ann Kim	PD3'	285	49	164	114	10.61	25	365	1.6	
18	MCPSCPD10 P01	Ann Kim	PD3'	229	241	179	202	10.36	20	300	1.0	
19	HPLAJ24S11RPO2	JM	5671									N
20	HPLAJ24S11FPO1	JM	5672	48	24	18	19	10.32	20	230	6.5	
21	HPLAJ24S26FPO1	JM	5672	65	24	23	26	10 36	20	320	2.2	
22	HPLAJ24S32FPO1 39 FPO1	JM	5672									N
23	HPLAJ24S39FPO1 32 FPO1	JM	5672	80	61	45	60	10.43	15	35	1.3	
24	STCMT02Rp01a	QQZ	1548									N
25	STCMT02Rp01b	QQZ	1549									N
26	STCMT03Rp01a	QQZ	1548									N
27	STCMT03RP01b	QQZ	1549									N
28	STCMT06RP01a	QQZ	1548									N
29	STCMT06RP01b	QQZ	1549	53	53	33	23	10.41	50	270	1.9	
30	STCMT07RP01a	QQZ	1548									N
31	STCMT07RP01b	QQZ	1549									N
32	STCMT08RP01a	QQZ	1548									N

Analyzed by: __JPF__

Uploaded by: __JF__ Folder: __Scientist Folder__

Additional Comments: full length

Factura/Blast Analysis: _____

Human Genome Sciences, Inc.

Plate I.D.(s) _Fwd #1 / rev_

Date Initiated: _3/12/94_
Date Completed: _3/13/94_

Results Folder: _HGS 38 3/13/94_

% Good: _2/72 - 62%_   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: _Manual_	Machine ID: _38_
Prep Person:	Prep Person: _DMD_	Gel Loader: _KMC_
Prep Date:	Prep Date: _3/12/94_	Run Date: _3/12/94_

	#	Sample Name	Scientist name/init control	Primer DP/DT DP For	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	# Ns	Trash Code
A1	1	pgemf			549	326	150	192	9.24	54	670	3	
B1	2	BMP01F	JPW	Forwa	190	77	107	72	-12.00	-	.		R
C1	3	BMP02F	JPW	Forwa	457	201	174	169	9.43		105-290	6	
D1	4	BMP03F	JPW	Forwa	365	130	163	164	9.45		105-365	9	
E1	5	BMP06F	JPW	Forwa	250	155	141	127	-12.00	--	-	-	R
F1	6	BMP07F	JPW	Forwa	279	40	51	119	9.65		-	-	H
G1	7	BMP08F	JPW	Forwa	334	152	155	122	9.47		93-290	13	
H1	8	BMP09F	JPW	Forwa	279	125	135	134	9.42		60-	-	L
A2	9	BMP10F	JPW	Forwa	252	116	169	106	-12.00	-	-	-	R
B2	10	BMP11F	JPW	Forwa	266	176	106	171	9.64		111-655	11	
C2	11	BMP12F	JPW	Forwa	298	192	135	133	9.43		105-440	10	
D2	12	BMP13F	JPW	Forwa	392	206	169	150	9.30		95-440	15	
E2	13	BMP14F	JPW	Forwa	501	223	156	179	9.56		100-520	7	
F2	14	BMP15F	JPW	Forwa	461	238	135	174	9.65		100-630	8	
G2	15	BMP16F	JPW	Forwa	96	105	113	55	9.52		-	-	M
H2	16	BMP17F	JPW	Forwa	122	76	38	30	-12.00	-	-	-	R
A3	17	BMP18F	JPW	Forwa	373	196	144	123	9.48		95-440	12	
B3	18	BMP19F	JPW	Forwa	137	74	50	40	9.49		-	-	R
C3	19	BMP20F	JPW	Forwa	53	30	30	23	-12.00	-	-	-	H
D3	20	HPLAJ24S11F	JM (T22rr)	Forwa	169	51	67	63	9.26	63	70-355		25 poly T's
A10	21	HL1SB62Fa	D.KOZAK	Forwa		NO	ANALYZED	DATA				N	
A5	22	PGEMR	control	DP rev	503	342	225	187	9.43	77	670	5	
B5	23	HFSBC6527R	PLHUDSO	REV	90	47	51	36	-12.00	105	-	-	SFS
C5	24	HFSBC6533R	PLHUDSO	REV		NO	ANALYZED	DATA					N
D5	25	HUKBA46Ra	D.KOZAK	Rever	371	119	159	138	9.45	103	600	8	
E5	26	HTPAN08S03R	ANN KIM	Rever	225	169	91	76	9.30	105	150	10	
F5	27	HTPAN08S04R	ANN KIM	Rever	439	285	167	111	9.44	107	550	8	
G5	28	HTPAN08S13R	ANN KIM	Rever	119	85	60	46	9.40	110	130-455		20 poly T
H5	29	HTPAN08S14R	ANN KIM	Rever	346	217	124	102	9.43	106	605	4	
A6	30	HOSAB71Ra	ANN KIM	Rever	127	131	58	76	9.34	104	460	.	
B6	31	HE9MF72AR	ANN KIM	Rever	50	87	59	43	9.32	107	460	2	
C6	32	HE9MF73BR	ANN KIM	Rever	104	83	44	36	9.33	107	455	1	

Analyzed by: _D._
Uploaded by: _R._   Folder: _full length + scientists_
Factura/Blast Analysis: _____

Additional Comments: All the BMP samples have strong fluorescent stops in between 70-100.

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Human Genome Sciences, Inc.

Plate I.D.(s) _____ nuxc dts # 2

Date Initiated: 3/12/94

Results Folder: HGS 35 3/13/94

Date Completed: _____

% Good: 15/32   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: Manual	Machine ID: 35
Prep Person:	Prep Person: DMD	Gel Loader: DMD
Prep Date:	Prep Date: 2/12/94	Run Date: 3/12/94

#	Sample Name	Scientist name/init control	Primer DP/DT DT	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	PGEMDT			446	334	228	281	a.15	≈10	380	0N	
2	HMP8B73RP01	H.LI	1031	32	63	29	57	-12				R
3	HMP8B73FP01	H.LI	1030	26	38	45	77	-12				R
4	HWFBD68FP01	H.LI	3-3	20	186	202	152	-12				R
5	HWFBD68RP01	H.LI	3-4	12	32	62	51	-12				R
6	HEPBO63RP01	D.KOZAK	53-3	122	127	67	82	9.04	≈10	230	4N	
7	HL1SB62RP01	D.KOZAK	53-3									N
8	HSA8F11RP01	D.KOZAK	1339	174	142	84	77	9.11	≈20	230	8N	
9	HOSA871RP03	ANN KIM	55-3									N
10	HOSA871RP04	ANN KIM	5677									N
11	HOSA871RP06	ANN KIM	5637	18	48	31	24	-12				R
12	HE9MF73ARP03	ANN KIM	54-3									N
13	HE9MF73BRPO3	ANN KIM	55-3									N
14	HE9MF73ARP04	ANN KIM	5677									N
15	HE9MF73BRP04	ANN KIM	5677									N
16	HE9MF73ARP06	ANN KIM	5637									N
17	HE9MF73BRP06	ANN KIM	5637	18	50	29	23	-12				many N's
18	HTPAN08RP06	ANN KIM	56-5	243	172	285	202	9.04	≈40	340	2N	
19	HTPAN08RP07	ANN KIM	5633	474	424	655	204	9.12	≈50	240	8N	
20	MCPSCPD10P02	ANN KIM	PD 3	419	613	492	434	-12	≈90	180	3N	
21	HAPATPD10P02	ANN KIM	PD 3	384	512	280	190	9.12	≈30	260	9N	
22	HPLBTS2ARP01	ANN KIM	5635	237	400	293	157	9.00	≈130	280	2N	
23	HPLBTS2BRP01	ANN KIM	5635	242	301	199	125	9.10	≈10	300	6N	
24	HE2BG16RP01	ZHEN LI	1434									N
25	HE2BG16FP01	ZHEN LI	1432									N
26	HE2BG16RP02	ZHEN LI		269	260	210	121	9.11	≈20	270	2N	
27	HASSB35S08FP05	ZHEN LI	5634	172	91	44	61	9.06	≈40	200	11N	
28	HHPEC49S03FP14A	SUK		155	167	117	64	9.06	≈20	370	6N	
29	HHPEC49S03RP14A	SUK		113	63	78	66	9.12	≈80	250	1N	
30	HHPEC49S03FP15	SUK		50	46	42	20	9.14	≈50	150	4N	
31	HHPEC49S03RP15	SUK		57	71	49	30	9.05				many N's
32	HSSAW84S02P01	YWEI		92	95	79	53	9.09	≈50	300	4N	

Analyzed by: ASP   Factura/Blast Analysis: _____

Uploaded by: ASP   Folder: will be left t scientist

Additional Comments:

33

Applied Biosystems

Synthesis Order - 5756 HTPAN08R 124A-P08

Run date: 3/11/94
Run ID: 5756 AMK
Customer: Ann Kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 5756 HTPAN08R 124A-P08
Sequence: CTG GTC AAG TGG TAA GGA G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

34

Human Genome ~ences, Inc.

Date Initiated: 3/18/94

Date Completed: _____

Pla~ D.(s) _____DT's_____

Results Folder: _____ƒGS 10 3/19/94_____

% Good: _17/30_ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method:	Machine ID: 10
Prep Person:	Prep Person:	Gel Loader: SUBA
Prep Date:	Prep Date:	Run Date: 3/18/94

#	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trasl Code
1-A9	PGEMDT	CONTRO		89	987	575	162	10.51		550	0	
2-B9	7TMD126ARP01	ANN KIM	5780		NO	DATA						N
3-C9	7TMD126BRP01	ANN KIM	5780									N
4-D9	7TMD127ARP01	ANN KIM	5781	19	21	42	16	-12				R/L
5-E9	7TMD127BRP01	ANN KIM	5781									N
6-F9	7TMD130ARP01	ANN KIM	5782									N
7-G9	7TMD130BRP01	ANN KIM	5782		NO	DATA						N
8-H9	7TMD134BRP01	ANN KIM	5783									N
9-A10	7TMD136ARP01	ANN KIM	5784									N
10-B10	7TMD137ARP01	ANN KIM	5785	13	22	37	15	9.2				R/L
11-C10	7TMD137BRP01	ANN KIM	5785	35	98	98	27	10.15		370	4%	
12-D10	7TMD139ARP01	ANN KIM	5786	44	101	62	44	10.41		350	2%	
13-E10	7TMD139BRP01	ANN KIM	5786	30	68	98	35	10.39		350	<19	
14-F10	HTPAN08S03RP08	ANN KIM	5756		NO	DATA						N
15-G10	HTPAN08S03RP08 H-104	ANN KIM	5756		NO	DATA						N
16-H10	HTPAN08S13RP08	ANN KIM	5756		NO	DATA						N
17-A11	HTPAN08S14RP08	ANN KIM	5756		NO	DATA						N
18-B11	HTPAN08RP08	ANN KIM	5756		NO	DATA						N
19-C11	HSCBB75S03RP01a	MAC	5731	87	177	221	106	10.35		370	2%	
20-D11	HSCBB75S03RP01b	MAC	5731	76	158	166	89	10.29		370	1%	
21-E11	HSCBB75S03RP02a	MAC	5732	120	249	273	83	10.40		370	4%	
22-F11	HSCBB75S03RP02b	MAC	5732	120	209	239	76	10.34		380	4%	
23-G11	HSCBB75S03RP03a	MAC	5734	116	286	282	141	10.51		390	1%	
24-H11	HSCBB75S03RP03b	MAC	5734	70	152	187	85	10.51		360	1%	
25-A12	HSCBB75S03RP04a	MAC	5795	100	224	302	93	10.31		370	1%	
26-B12	HSCBB75S03RP04b	MAC	5795	108	334	318	97	10.26		380	2%	
27-C12	HSCBB75S03RP05a	MAC	5796	51	196	196	89	10.41		250	5%	
28-D12	HSCBB75S03RP05b	MAC	5796	63	134	154	70	10.47		250	5%	
29-E12	HSCBB75S03RP06a	MAC	5797	55	117	81	49	10.36		350	3%	
30-F12	HSCBB75S03RP06b	MAC	5797	51	100	139	45	10.40		350	3%	
31-G12												
32-H12												

Analyzed by: Donna

Uploaded by: Donna Folder: Sci/Full length

Additional Comments:

Factura/Blast Analysis: _____

NO REDO's

for #6 ~ DNA should be 04
G10 (wrong scienan tube)

35

Human Genome Sciences, Inc.

Plate I.D.(s) *manuels*

ate Initiated: _____

Date Completed: _7/22/94_

Results Folder: _07/22/94 17 HGS_

% Good: _50_   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:MISC	Method:BIOMEK/MANUAL	Machine ID: _17_
Prep Person:MISC	Prep Person:ASP	Gel Loader: _ASP_
Prep Date:MISC	Prep Date:07/21/94	Run Date: _07/21/94_

#.	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength G	A	T	C	Base Spacing	Vector	Edited length	% N	Trash Code
1-A1	PGEMDT	CONTRO	DT	99	164	139	89	9.52	50	390	0	
2-B1	HTPAN08S04RP01a	Ann Kim		168	698	178	63	9.50	70	240	2.9	
3-C1	HTPAN08S04RP03a	Ann Kim		221	218	300	56	9.59	70	240	.8	
4-D1	HTPAN08S04RP05a	Ann Kim		165	453	18	63	9.41	80	280	1.4	
5-E1	HTPAN08S04RP06a	Ann Kim		110	531	185	85	9.43	60	100	15	
6-F1	HTPAN08S04RP07a	Ann Kim		185	139	240	50	9.53	70	270	.33	
7-G1	HTPAN08S04RP09a	Ann Kim										N
8-H1	HTPAN08S04RP10a	Ann Kim		120	197	103	74	9.29	80	380	0	
9-A2	HTPAN08S04RP12a	Ann Kim		222	461	188	80	9.29	80	330	.6	
10-B2	HTPAN08S04RP14a	Ann Kim		217	141	221	89	9.44	70	330	.9	
11-C2	HTPAN08S04FP15a	Ann Kim		175	134	200	56	9.43	80	270	33	
12-D2	HTPAN08S13RP01a	Ann Kim		74	59	58	105	-12.00				R
13-E2	HTPAN08S13RP03a	Ann Kim										N
14-F2	HTPAN08S13RP05a	Ann Kim										N
15-G2	HTPAN08S13RP06a	Ann Kim										N
16-H2	HTPAN08S13RP07a	Ann Kim										N
17-A3	HTPAN08S13RP09a	Ann Kim		133	117	99	49	9.35	70	390	2.6	
18-B3	HTPAN08S13RP10a	Ann Kim										N
19-C3	HTPAN08S13RP12a	Ann Kim		21	49	57	62	-12.00				R
20-D3	HTPAN08S13RP14a	Ann Kim										N
21-E3	HTPAN08S13EP15a	Ann Kim										N
22-F3	HHCMF74FP11	SUK		239	260	176	113	9.35	80	360	.6	
23-G3	HHCMF74RP11	SUK		191	155	216	107	9.40	70	310	1.6	
24-H3	HHCMF74FP12	SUK		280	290	121	89	9.41	70	390	0	
25-A4	HHCMF74FP13	SUK		281	411	155	101	9.44	90	300	0.3	
26-B4	HHCMF74FP14	SUK		213	318	144	85	9.28	30	350	1.7	
27-C4	HHCMF74RP12	SUK		194	175	186	76	9.37	50	340	0.3	
28-D4	HHCMF74FP01B	SUK		224	218	250	80	9.46	20	400	0.3	
29-E4	HMSBX93FP01B	SUK		223	233	249	80	9.52	50	400	0.5	
30-F4	HNFAG09FP01B	SUK		81	66	51	31	9.62	40	480	0.6	
31-G4	HP16A2A	Laurie										N
32-H4	HP2A2D	Laurie										N

Retracked ASP

Analyzed by: ____

Uploaded by: _ASP_   Folder: _Full length_

Factura/Blast Analysis: ____

+ scientists

ПТ 1-3 ... ASP

36

Applied
Biosystems

Synthesis Order - 6442 HTPAN08 SCREEN RP01

Run date: 5/4/94
Run ID: 6442
Customer: ANN KIM

RP02

1.   CX
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: HTPAN08 SCREENRP01
Sequence: GCA GAT GCA GGA CAA GTA C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
  Sent to "Synthesizer-1" col 3 seq 33 at 5/5/94 10:19 AM.

Sequence
HTPAN08
504
514

RP10

37

(Peptide) TFASTA of: U03470.Gp_All   from: 1 to: 278   May 5, 1994   11:39

```
.OCUS         RNU03470_1 .
DEFINITION    Rattus norvegicus Fas antigen ligand mRNA, complete cds. Ligand
              for Fas antigen; A member of TNF-family; apoptosis-inducing
              capacity; typeII-transmembrane protein; ligand for receptor.
              NCBI gi: 440179.
DATE          12-JAN-1994 . . .
```

TO: contig1.seq Sequences: 1 Symbols: 1,872 Word Size: 2

The best scores are: frame init1 initn opt

1Dual:[Hgs.Ruben]Contig1.Seq	REFORMAT of: Contig1.Seq...(3)	86	123	197
1Dual:[Hgs.Ruben]Contig1.Seq	REFORMAT of: Contig1.Seq...(1)	32	32	54
1Dual:[Hgs.Ruben]Contig1.Seq	REFORMAT of: Contig1.Seq...(6)	32	32	42
1Dual:[Hgs.Ruben]Contig1.Seq	REFORMAT of: Contig1.Seq...(4)	31	31	50
1Dual:[Hgs.Ruben]Contig1.Seq	REFORMAT of: Contig1.Seq...(5)	29	29	36
1Dual:[Hgs.Ruben]Contig1.Seq	REFORMAT of: Contig1.Seq...(2)	28	28	35

```
U03470.Gp_All
$1$Dual:[Hgs.Ruben]Contig1.Seq

 REFORMAT of: Contig1.Seq  check: -1  from: 1  to: 1876  May 5, 1994  11:38
(No documentation)
```

CORES   Frame: (3) Init1: 86 Initn: 123 Opt: 197
           24.1% identity in 170 aa overlap

```
            90        100       110       120       130       140
U03470  FFMVLVALVGMGLGMYQLFHLQKELAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSV
                    : ::|  |  :| |:   ::   :::::::: :|
Contig  KSSGTPSARXKDDFENLXGNHFYSSRKATKYLSPSERKRSSESSSSHNWDQRKNNTLSSP
           180       190       200       210       220       230

           150       160       170       180       190       200
U03470  AHLTGNPRSRSIPLEWEDT-YGTALISGVKYKKGGLVINEAGLYFVYSKVYFR-GQSCNS
        :  ::::: :|:|   :||::   | :::|::: ::|:|||:| |:|::||::|||  :: ::
Contig  NSKNEKALGRKIN-SWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKE
           240       250       260       270       280       290

           210       220       230       240       250
U03470  QPLSHK---VYMRNF-KYPGDLVLMEEKKLN-YCTTGQIWAHSSYLGAVFNLTVADHLYV
        :: ::|     |: ::  :||: ::||::  :  :  ::::::::    :| | |::|:|: :|::  |
Contig  NTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRILV
           300       310       320       330       340       350

           260       270
U03470  NISQLSLINFEESKTFFGLYKL
        ::::  ||::::::  :|||  :
Contig  SVTNEHLIDMDHEASFFGAFLVGXLTWKEKAITSKXLFSFQDDTLXRCFKKSDQNKQTEN
           360       370       380       390       400       410
```

```
·03470.Gp_All
,1$Dual:[Hgs.Ruben]Contig1.Seq

 REFORMAT of: Contig1.Seq  check: -1  from: 1  to: 1876  May 5, 1994  11:38
(No documentation)
```

SCORES   Frame: (1) init1: 32 Initn: 32 Opt: 54
          14.2% identity in 120 aa overlap

              40   50   60   70   80   90
'03470 PGQRRPPPPPPPPSPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLV-ALVGMGLGM
                    |: :: :|:|: : :   ::: ::   : |
Contig TLYCXXKVLEIVVGLKMQNMDSIPSIKGEYLSLRKMTEFWFLXQMSTXXTWTMKPVFSGP
              320   330   340   350   360   370

              100   110   120   130   140   150
U03470 YQLFHLQKELAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSVAHLTGNPRSRSIPLE
          ::| ::: :   :::: :   :|:   :|: | ::::: |: :: :   :::::|::   :
Contig FXLANXPGKKKQXPQSDYSVFRMIHYEDVSKNLTKTNKQKTENKKPSMQSEXSSHNQKIL
              380   390·   400   410   420   ·430

              160   170   180   190   200   210
U03470 WEDTYGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCNSQPLSHKVYMRNFKYPGD
          :: :::::|: | | |: : :||||::
·Contig QHTLFXKXLTYPKKMK---LLKDLSGLYLISVCXQKSRRLSASKHXCNGYIFWLYNLHLV ··
              440   450   ·   460   ·470   480

U03470.Gp_All
1Dual:[Hgs.Ruben]Contig1.Seq

REFORMAT of: Contig1.Seq check: -1 from: 1 to: 1876 May 5, 1994 11:38
(No documentation)

SCORES   Frame: (6) Init1: 32 Initn: 32 Opt: 42
          34.8% identity in 23 aa overlap

              230   240   250   260   270
·'03470 EKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNI-SQLSLINFEESKTFFGLYKL
                         :|::| |::: |: ||: | |
Contig PVPSGVNELDLEXMERPKASDFXFPXNVRSIYIHIYISLNFXVFDMSKNPFPLPXSLSET
              `550   560   570   580   590   600

Contig HEENCVSFKDVNXMIETCT
              610   · 620

U03470.Gp_All
1Dual:[Hgs.Ruben]Contig1.Seq

REFORMAT of: Contig1.Seq. check: -1 from: 1 to: 1876 May 5, 1994 11:38
(No documentation)   `

SCORES   Frame: (4) Init1: 31 Initn: 31 Opt: 50
          16.7% identity in 102 aa overlap

                              10   20   30   40
U03470   MQQPVNYPCPQIYWVDSSATSP-WAPPGSVFSCPSSGPRGPGQ
                           |:::: | :::::|:::: : |:: |
Contig RHWGPNNCHLLLRNKQCHFWSTCPASASARWXSTRKLQPHRETAGALXRFTISTQVCPRL
              470   480   490   500   510   520

              50   60   70   80   90   100
U03470 RRPPPPPPPPSPLPPPSQPPPLPPLSPLKKKD-NIELWL-PVIFFMVLVALVGMGLGMYQ
          :| ||::|::   : :: ::| ::|:|| ::: ::: | :   ::: : :::: : :|
Contig VPPGPPSXPXTCQSLTAVSQPGSRLCPLGXMSLTXSKWRDQKPLIFNFHKMLEVYIYIYI
              530   540   550   560   570   580

              110   120   130   140   150   160
U03470 LFHLQKELAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSVAHLTGNPRSRSIPLEWE
          :::: ::| |:
Contig FLXIFESLICLKIHSLCPEAXVRHMKKTVFHLKMLIKXLKLVL

U03470.Gp_All
^1$Dual:[Hgs.Ruben]Contig1.Seq

REFORMAT of: Contig1.Seq check: -1 from: 1 to: 1876 May 5, 1994 11:38
(No documentation)

SCORES   Frame: (5) Init1: 29 Initn: 29 Opt: 36
            11.1% identity in 27 aa overlap

```
         50        60        70        80        90       100
U03470 PPPPPSPLPPPSQPPPLPPLSPLKKKDNIELWLPVIFFMVLVALVGMGLGMYQLFHLQKE
                              :||  :::    :  :::    :  ::  |  ::
Contig DMRXSPERSFSNFIFLGXVSHFQNSVCCRIFWLWLLYSDCIEGFLFSVFCLFVLVRFFET
         170       180       190       200       210       220


         110       120       130       140      150       160
U03470 LAELREFTNHSLRVSSFEKQIANPSTPSETKKPRSVAHLTGNPRSRSIPLEWEDTYGTAL

Contig SSXCIILKTEXSLXGYCFFFPGQLANXKGPEKTGFMVHVYQVLICYRNQNSVIFLKLKYS
         230       240       250       260       270       280
```


U03470.Gp_All
1Dual:[Hgs.Ruben]Contig1.Seq

REFORMAT of: Contig1.Seq check: -1 from: 1 to: 1876 May 5, 1994 11:38
(No documentation)

SCORES   Frame: (2) Init1: 28 Initn: 28 Opt: 35
            16.7% identity in 18 aa overlap

```
         160       170       180       190       200       210
U03470 EDTYGTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQSCNSQPLSHKVYMRNFKYPGDL
                             :|  :::::::::|::|  ::
Contig MKMFQKIXPKQTNRKQKTKNPLCNLSRAATTKKFYNTHCSESDSLIPRKXNCXKIFQDST
         400       410       420       430       440       450


         220       230       240       250       260       270
U03470 VLMEEKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFGLYKL

Contig SYQFASRNLEDCQLPNINAMVTSSGFIIYTLXRLXKKAQQSISQVVYHSSSLQVSLRDNI
```

Applied Biosystems

Synthesis Order - 6445 HTPAN08S13R P01

Run date: 5/6/94
Run ID: 6445 AMK
Customer: ann kim

1.   KH
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 6445 HTPAN08S13 RP01
Sequence: TGT CTC ACT CAG GCT TCA G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

RP01
RP09

Comments:

RP09

41

Human Genome ~iences, Inc.

Date Initiated: 05/11/94 _____
Date Completed: __05/12/94__

Results Folder: __C5/12/94 x9 HG5__ ✓
13/26 = 50%
% Good: __13/26 = 50%__ % Good: _____

	Templates		Sequence Reaction		Gel Run
Method:			Method: MANUALS		Machine ID: _19 4C_
Prep Person:			Prep Person: JMA		Gel Loader: JMA
Prep Date:			Prep Date: 05/11/94		Run Date: 05/11/94

G A T C

#	Sample Name	Scientific name/init	Primer DP/DT	C	A	G	T	Base Spacing	Vector	Edited Length	Ns	Trash Code
A1	PGEM	control	DT	178	170	130	64	12.05	38	432	2N	
B1	SOL10FFa	A.Chopra		160	149	98	65	12.11	20	310	7N	
C1	SOL10RFa	A.Chopra		—	—	—	—	—				N ✳
D1	TNFQE60NB1P01 a	A KIM		54	64	48	30	12.08	80	320	8N	
E1	TNFQE60NB2P01 a	A KIM		66	85	54	34	12.05	50	380	12N	
F1	TNFQE60NB3P01 a	A KIM		34	39	2C	21	11.91				K
G1	TNFQE60BN4P01 a	A KIM		72	87	56	35	11.98	40	390	6N	
H1	TNFQE60BN5P01 a	A KIM		133	195	109	63	11.99	20	430	4N	
A2	TNFQE60BN6P01 a	A KIM		46	56	37	25	11.99	70	300	6N	
B2	HTPAN08S04RP01 a	A KIM		142	303	176	62	11.98	40	390	4N	
C2	HTPAN08S13RP01 a	A KIM		—	—	—	—	—				N ✳
D2	HTPAN08S14RP01 a	A KIM		107	224	129	48	12.01	40	390	5N	
E2	HPRBI22RP01 a	BEDNARI		65	85	69	32	12.02	48	378	5N	
F2	HFCSA70RP01 a	BEDNARI		—	—	—	—	—				N
G2	HSAID14RP01 a	BEDNARI		51	47	39	26	12.09	50	250	5N	
H2	HLTAF30RP01 a	BEDNARI		54	50	65	40	11.99	50	180	2N	
A3	HLTBR87RP01 a	Bednarik		—	—	—	—	—				N
B3	HPDEF51RP01 a	Bednarik		40	36	30	20	11.72	40	94	2N	
C3	HTPAN18S40RP01 a	Bednarik		—	—	—	—	—				N
D3	HPTTT24S3FP03 a	meissner		333	185	665	371	11.89				H ✳
E3	HUVCT01S02RP01 a	HASTING		—	—	—	—	—				N
F3	HUVCT01S02RP02 a	HASTING		—	—	—	—	—				N
G3	HUVCT01S02FP01 a	HASTING		—	—	—	—	—				N
H3	HUVCT01S03RP01 a	HASTING		—	—	—	—	—				N
A4	HUVCT01S03RP02 a	HASTING		15	55	52	29	-12.00				K
B4	HUVCT01S03FP01 a	HASTING		—	—	—	—	—				N
27	K a											
28												
29												
30												
31												
32												

Analyzed by: _JMA_
Uploaded by: _JMA_ Folder: _FULL LENGH_
Additional Comments: SCIENTISTS
SEQ.

Factura/Blast Analysis: _____

✳ SUBMIT FOR REDO

Applied Biosystems

Synthesis Order - 6638 HTPAN08FULLR 362S P02

Run date: 5/19/94
Run ID: 6638 ak
Customer: ANN KIM

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 6638 HTPAN08FULLR 362S P02
Sequence: CTG CAG TCT CTC TGT GTG G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
Sent to "Synthesizer-2" col 3 seq 33 at 5/23/94 9:16 AM.

P12

X

43

Synthesis Order - 6639 HTPAN08FULLR 433A P03

Run date: 5/19/94
Run ID: 6639 ak
Customer: ANN KIM

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 6639 HTPAN08FULLR 433A P03
Sequence: GTA CTT GTC CTC CAT GTG C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
  Sent to "Synthesizer-2" col 4 seq 34 at 5/23/94 9:18 AM.

ab *Applied Biosystems*

Synthesis Order - 6640 HTPAN08FULLR 783A P04

P14

Run date: 5/19/94
Run ID: 6640 ak
Customer: ANN KIM

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 6640 HTPAN08FULLR 783A P03
Sequence: GAA TGC CCA CTC CTT GAT G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-1" col 1 seq 31 at 5/23/94 9:19 AM.

Human Ge~ ~e Sciences, Inc.   ~e I.D.(s) _____ _____

Date Initiated: 5/20/94 _____

Results Folder: __05/21/94 38 HGS__

Date Completed: _____

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 38
Prep Person:	Prep Person: DS	Gel Loader: DS
Prep Date:	Prep Date: 5/20/94	Run Date: 5/20/94

#	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	# ol No.	Trash Code
1-A1	PGEMR lane B	control	DP	347	191	119	172	9.95		360	5	
2-B1	HTPAN08Rc	ANN.KIM	REV	449	176	222	184	10.01	95	340	0	
3-C1	HTPAN08S04Rc2	ANN.KIM.	REV	303	186	170	158	10.07	95	350	5	
4-D1	HTPAN08S13Rc	ANN.KIM	REV	194	69	64	59	10.11	90	420	6	
5-E1	HETAS76Rc	ANN.KIM	REV	143	67	118	71	10.03				A CF
6-F1	HETAQ44Rc	ANN.KIM	REV	430	198	163	150	10.07	95	350	1	
7-G1	HTHBC32R	HLI	REV	101	63	46	55	10.09	90	420	2	
8-H1	HIBEB91R2	LINSCOR	REV	251	137	110	84	10.00				H
9-A2	HLHBD62R2	LINSCOR	REV	224	208	171	159	10.04	100	270	3	
10-B2	FB2A1R	LINSCOR	REV	433	277	160	122	10.06	95	370	1	
11-C2	FB1181R	LINSCOR	REV	280	206	106	97	10.03	90	400	0	
12-D2	FB11B2R	LINSCOR	REV	424	257	149	137	10.05	95	350	0	
13-E2	FB1401R	LINSCOR	REV	423	324	180	184	10.01	95	350	0	
14-F2	FB18A1R	LINSCOR	REV	538	215	246	182	10.06	100	410	1	
15-G2	HUVCT01S04RA	GAH	REV									nc primer
16-H2												nc primer
17-A3	PGEMF	control	FOR	306	159	169	152	10.09		360	2	
18-B3	HTPAN08Fc	ANN.KIM	FOR	358	155	234	158	10.07				R
19-C3	HTPAN08S04Fc2	ANN.KIM	FOR	178	69	152	73	10.07				R
20-D3	HTPAN08S13Fc	ANN.KIM	FOR	121	47	96	69	10.11				AMi
21-E3	HETAS76Fc	ANN.KIM	FOR	158	95	56	74	10.10	80	370	3	Rev
22-F3	HETAQ44Fc	ANN.KIM	FOR	246	120	162	112	10.00				F
23-G3	HTHBC32F	HLI	FOR	92	47	52	53	12.00				R
24-H3	FB2A1F	LINSCOR	FOR	206	105	146	112	9.96				R
25-A4	FB1181F FB1181F	LINSCOR	FOR	363	152	277	132	9.76				A
26-B4	FB11B2F FB11B1F	LINSCOR	FOR	331	137	191	129	10.05	40	320	15	A
27-C4	FB1401F	LINSCOR	FOR	477	344	368	222	9.96	40	290	5	
28-D4	FB18A1F	LINSCOR	FOR	604	295	291	163	10.00	40	370	4	
29-E4												
30-F4												
31-G4												
32-H4												

Analyzed by: _Alice_

Uploaded by: _HGS_

Folder: _1994 Scarlet Full length_

Factura/Blast Analysis: _____

Additional Comments:

Weak signals on Rows 15, May 23

- HUVCT01 S04RA not enough to rxn resultant
- Linscor samples - need to add at least .5 ul per Rxn - please send proper amount and Tin.
- HLI - only real please send .5 ul per RXN

Human Ge___ne Sciences, Inc. Plate I.D.(s___ ᴧANUAL DTS_____ _____

Date Initiated:05/20/94 _____

Date Completed: 05/21/94 _____

Results Folder: 05121|GH 35 HGS

% Good: 13/24 % Good:_____

Templates	Sequence Reaction	Gel Run
Method:MISC	Method:BIOMEK/MANUAL	Machine ID: 35
Prep Person:———	Prep Person:TAL	Gel Loader: CDL
Prep Date:———	Prep Date:05/20/94	Run Date: 5|20|94

#	Sample Name	Scientist name/init.	Primer DP/DT DT	Signal Strength G	A	T	C	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	PGEMDT	control	DT	53	130	100	59	9.07	40	450	2N	
2-B5	HTPAN08S04RP05	A KIM	5426	188	124	222	69	9.03	40	390	6.01	
3-C5	HTPAN08S04RP06	A KIM	5676	170	607	178	72	9.03	40	350	3N	
4-D5	HTPAN08S04RP07	A KIM	5688	210	191	375	62	9.04	40	370	16N	(N)
5-E5	HTPAN08S04RP10	A KIM	6442	155	391	132	54	9.03	100	350	7N	
6-F5	HTPAN08S13RP01	A KIM	685									N
7-G5	HTPAN08S13RP03b	A KIM	5424									N
8-H5	HTPAN08S13RP05	A KIM	5426									N
9-A6	HTPAN08S13RP06	A KIM	5676									N
10-B6	HTPAN08S13RP07	A KIM	5688									N
11-C6	HTPAN08S13RP09	A KIM	6445	91	101	81	37	9.00	40	380	5N	
12-D6	HTPAN08S13RP10	A KIM	6442	12	25	24	36	-12				R
13-E6	HETAS768RP01	A KIM	5809									N
14-F6	HETAS768RP02	A KIM	6152									N
15-G6	HETAQ44RP01	A KIM	5810									N
16-H6	HETAQ44RP02	A KIM	6151									N
17-A7	HARAG42RP01	A. Politis	6575	35	38	29	16	9.00	100	90	4	(H)
18-B7	HTABK03RP04	CRG	6557									N
19-C7	HTABK03FP03	CRG	6558									N
20-D7	HUVCT01S04RP04	GAH	6563	37	113	123	45	9.00	70	320	12N	
21-E7	HUVCT01S04FP05	GAH	6553	250	149	135	105	9.00	40	420	9 1N	
22-F7	HUVCT01S04FP06	GAH	6554	106	131	192	74	9.00	50	460	11N	
23-G7	HUVCT01S04FP07	GAH	6562	151	231	231	82	9.00	80	320	14N	
24-H7	HE9NG77RP02	GAH	6565	65	74	70	25	9.00	40	300	7N	
25-A8	HE9NG77FP03	GAH	6564	178	129	157	47	9.00	50	375	2N	
26-B8	HE9NG77FP04	GAH	6567	134	120	108	55	9.00	70	370	2N	
27-C8	HE9NG77FP05	GAH	6566	121	158	157	44	9.00	100	375	2N	
28-D8	HFGAN72S04FP02	SOPPET	6358									N
29-E8												
30-F8												
31-G8												
32-H8												

Analyzed by: TCB
Uploaded by: TCB Folder: full length Factura/Blast Analysis: _____
Scientist
Additional Comments:

Human Gene Sciences, Inc. Plate I.D.(s) _ ANUAL DTS_____

Date Initiated: 5/20/94 _____ Results Folder: 05/21/94 39 HGS

Date Completed: 5/21/94 _____ % Good: 14/32 % Good: _____

Templates	Sequence Reaction	Gel Run
Method: MISC.	Method: BIOMEK/MANUAL	Machine ID: 39
Prep Person: ——	Prep Person: TAL	Gel Loader: CDL
Prep Date: ——	Prep Date: 5/20/94	Run Date: 5/20/94

#	Sample Name	Scientist name/init control	Primer DP/DT	Signal Strength G	A	T	C	Base Spacing	vector	Edited length	% N's	Trash Code
1-A1	PGEMDT	control	DT	291	338	213	86	9.87	20	530	2N	
2-B1	HTOAE49RP05	CRG	6585	264	205	121	66	9.89	20	400	1N	
3-C1	HTOAE49RP06	CRG	6586	291	191	101	68	9.92	20	380	5N	
4-D1	HPRTK95S01FP04	FISCHER	6129									N
5-E1	HPRTK95S02FP04	FISCHER	6129									
6-F1	HPRTK95S05FP04	FISCHER	6129									
7-G1	HPRTK95S06FP04	FISCHER	6129									
8-H1	HPRTK95S08FP04	FISCHER	6129									
9-A2	HPRTK95S14FP04	FISCHER	6129									
10-B2	HPRTK95S15FP04	FISCHER	6129									
11-C2	HPRTK95S03FP04	FISCHER	6129									
12-D2	HPRTK95S01RP01	FISCHER	5988									
13-E2	HPRTK95S02RP01	FISCHER	5988									
14-F2	HPRTK95S05RP01	FISCHER	5988									
15-G2	HPRTK95S06RP01	FISCHER	5988									
16-H2	HPRTK95S08RP01	FISCHER	5988									
17-A3	HPRTK95S14RP01	FISCHER	5988									
18-B3	HPRTK95S15RP01	FISCHER	5988									
19-C3	HPRTK95S03RP01	FISCHER	5988									✓
20-D3	HTPAN08RP01b	A KIM	685	262	827	330	721	9.85	136	200	6N	light
21-E3	HTPAN08RP03b	A KIM	5424	180	200	170	48	9.82	20	290	2N	
22-F3	HTPAN08RP05b	A KIM	5426	294	822	408	1A	9.52	40	270	kN	high luc
23-G3	HTPAN08RP06b	A KIM	5676	191	1684	256	91	9.75	60	340	3N	
24-H3	HTPAN08RP07b	A KIM	5688	230	254	349	73	9.52	60	300	4N	
25-A4	HTPAN08S04RP01	A KIM	685	237	344	304	112	9.78	60	300	11 N	
26-B4	HTPAN08S04RP03b	A KIM	5424	273	368	502	101	9.77	60	240	3N	O
27-C4	HTPAN08S04RP05	A KIM	5426	245	757	370	89	9.72	60	300	2N	high luc
28-D4	HTPAN08S04RP06	A KIM	5676	212	702	290	110	9.67	68	340	5N	
29-E4	HTPAN08S04RP07	A KIM	5688	200	277	361	84	9.71	60	340	8N	
30-F4	HTPAN08S04RP10	A KIM	6442	191	420	183	77	9.60	60	350	2N	
31-G4	HTPAN08S13RP01	A KIM	685									N
32-H4	HTPAN08S13RP03b	A KIM	5424									N

Analyzed by: _____

Uploaded by: _____ Folder: Sculp full

Additional Comments: _____

Factura/Blast Analysis: _____

no redos

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db Applied Biosystems

Synthesis Order - 6813 htpan08fp15

Run date: 6/7/94
Run ID: 6813 AMK
Customer: ann kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 6813 HTPAN08FP15 - 1520a
Sequence: TAC AGG CAT GTG CCA ACA C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

49

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Templates	Sequence Reaction	Gel Run
Method:	Method:MANUALS	Machine ID: 27
Prep Person:	Prep Person:JSS	Gel Loader: JSS
Prep Date:	Prep Date:6/08/94	Run Date: 6/8/94

#	Sample Name	Scientist name/init	Primer DF/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% N	Trash Code
1-A1	PGEMF	CONTR	FOR	17	21	17	13	-12				R
2-B1	HTPAN08S04Fd	ANN KIM	FOR	141	140	48	66	9.80	45			T
3-C1	HTPAN08S13Fd	ANN KIM	FOR	18	20	17	16	-12				R
4-D1	HTPAN08Fd	ANN KIM	FOR	247	219	125	127	9.85	49			T
5-E1	HE20I42Fb	ANN KIM	FOR	280	231	67	78	9.70	43/48	267	6N	
6-F1	HALSK38F	ANN KIM	FOR	65	266	128	128	9.83	43			M
7-G1	HOSAB71F	ANN KIM	FOR	43	35	19	17	9.85	41			L
8-H1	HE9MF73F	ANN KIM	FOR	311	144	103	141	9.86	44			R/T
9-A2	HPRBM59S01F	HLI	FOR	16	20	15	13	-12				R
10-B2	HPRBM59S02F	HLI	FOR	146	148	41	70	9.87	47			T
11-C2	HPRBM59S03F	HLI	FOR	68	71	23	26	9.81	48			T
12-D2	HPOAA65F	HLI	FOR									N
13-E2	HETCN46F	KOVACS	FOR	14	16	15	14	-12				R
14-F2	HNEAA81Fa	HLA	FOR	143	77	52	48	9.84	49			T
15-G2	PGEMR	CONTR	REV	25	20	17	14	-12				R
16-H2	HCACI93R	FISCHER	REV	200	138	40	66	10.00	107	233	3N	
17-A3	HIBECS2R	FISCHER	REV	84	32	24	25	9.83	43			R
18-B3	HETCN46Ra	KOVACS	REV	323	170	63	68	9.91	100	270	4N	
19-C3	HPRBM59S01R	HLI	REV	257	149	72	63	10.08	94	140	4N	
20-D3	HPRBM59S02R	HLI	REV	369	244	81	87	9.96	93			M
21-E3	HPRBM59S03R	HLI	REV	284	209	85	76	10.00	91			M
22-F3	HPOAA65R	HLI	REV									N
23-G3	HTPAN08S04Rd	Ann Kim	REV	290	218	77	64	10.06	97	253	7N	
24-H3	HTPAN08S13Rd	Ann Kim	REV	93	63	35	23	9.92	106	104	9W6N	
25-A4	HE20I42RB	Ann Kim	REV	438	311	111	114	9.93	95	270	N	
26-B4	HALSK38R	ANN KIM	REV	447	142	107	133	9.85	97	235	2N	
27-C4	HOSA871R	ANN KIM	REV	256	143	67	73	9.95	97	150	1N	
28-D4	HE9MF73R	ANN KIM	REV	326	226	81	61	9.80	103	240	9N	
29-E4	HSRDG78aR	REINER	REV	230	167	71	98	9.65	90	194	16N	
30-F4	HSRDG78bR	REINER	REV	312	244	99	97	9.76	92	208	10N	
31-G4	P161C2R	D.Kozak	rev	363	298	101	105	9.98	96	254	2N	
32-H4	P161C3R	D.Kozak	rev	90	51	35	27	9.85	95	205	5N	

Retracted → Julie

Analyzed by: _____ Julie   Factura/Blast Analysis: _____

Uploaded by: Julie   Folder: Full length + scientist

Additional Comments:

50

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: __06/09/94__

Results Folder: __06/09/94   35   HGS__

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 35
Prep Person:	Prep Person: MICHAEL	Gel Loader: Michael
Prep Date:	Prep Date: 06/08/94	Run Date: ~06/09/94

#	Sample Name	Scientist name/unit	Primer DP/DT	Signal Strength				Base Spacing	Vector	Edited Length	%GC/Nr	Trash Code
1-A1	PGEMDT	CONTROL	DT	197	168	113	65	10.19	10	370	2.3	
2-B1	HFGAN72S04CFP04A	soppet/gra	6685	124	130	99	44	10.30	40	300	8.3	
3-C1	HFGAN72S04CRP05A	soppet/gra	6681	117	84	62	54	10.02	60	230	11.3	
4-D1	HETCN46RP01	KOVACS	5458	236	255	174	57	10.24	30	350	4.3	
5-E1	HETCN46RP02	KOVACS	1511	159	187	138	61	10.01	40	360	3.5	
6-F1	HETCN46RP03	KOVACS	6150	134	157	147	63	10.19	30	230	2.3	
7-G1	HETCN46RP04	KOVACS	6632									N
8-H1	HETCN46FP01	KOVACS	6631	80	89	52	27	10.23	50			X
9-A2	HETCN46FP03	KOVACS	1509	74	89	67	36	10.11	50	350	4.5	
10-B2	HETCN46FP04	KOVACS	1510	133	124	90	46	10.09	30	320	6.3	
11-C2	HTABK03CRP04	CRG	6557									N
12-D2	HTABK03CFP03	CRG	6558									N
13-E2	HSNBL85ARP01	CRG	6694									N
14-F2	HTPAN08S04P12	Ann Kim	6638	265	66	258	97	9.86	30	330	—	
15-G2	HTPAN08S04P13	Ann Kim	6639									N
16-H2	HTPAN08S04P14	Ann Kim	6640	349	263	345	127	10.03	30	320	2.3	
17-A3	HTPAN08S13P12	Ann Kim	6638									N
18-B3	HTPAN08S13P13	Ann Kim	6639									N
19-C3	HTPAN08S13P14	Ann Kim	6670	—								N
20-D3	HE2OI42RP01	Ann Kim	6802	166	248	122	70	9.96	40	310	1.m	
21-E3	HE2OI42RP02	Ann Kim	6800									N
22-F3	HALSK38RP02	ANN KIM	5233									N
23-G3	HALSK38RP03	ANN KIM	5513	11	19	67	14	-12.00				R
24-H3	HALSK38RP04	ANN KIM	5677	10	15	59	13	12.00				R
25-A4	HOSAB71RP02	ANN KIM	5233	37	45	35	16	10.34	40	200	11.3	
26-B4	HOSAB71RP03	ANN KIM	5513									N
27-C4	HOSAB71RP04	ANN KIM	5677									N
28-D4	HOSAB71RP05	ANN KIM	5711	161	389	246	52	9.89	40	340	2.3	
29-E4	HOSAB71RP06	ANN KIM	5697									N
30-F4	HE9MF73RP02	ANN KIM	5233									N
31-G4	HE9MF73RP03	ANN KIM	5513	—								N
32-H4	HE9MF73RP04	ANNKIM	5677									N

Analyzed by: Michael

Uploaded by: Anna   Folder: Scientist/Allison

Factura/Blast Analysis: _____

π More primer peaks, overall weak gel

51

Human Genome Sciences, Inc.

Plate ..D.(s) _manuals_

Date Initiated: _6/10_   Results Folder: _06/11/94 38 HGS_

Date Completed: _6/13_   % Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 38
Prep Person:	Prep Person: DEBBIE	Gel Loader: ?
Prep Date:	Prep Date: 06/10/94	Run Date: 6/10/94

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	pgemdt	control	dt	115	241	286	216	13.67	20	390	0.8	
2-B1	HLHCT51POI'	LINSCOR	POI	145	200	257	171	13.42	40	400	6.0	
3-C1	VEGF2PF2'	LINSCOR	VEGFx	114	254	195	257	13.39	30	380	9.7	
4-D1	HTPAN08FP15	ANN KIM	6813	74	240	242	343	13.29	30	350	0.6	
5-E1	HTPAN08S04FP15	ANN KIM	6813	98	247	322	322	13.36	30	360	1.1	
6-F1	HTPAN08S13FP15	ANN KIM	• 6813	32	29	14	53	-12.00				R
7-G1	hhpsi84s13rp02	kinneret	dt	60	128	108	78	13.48	20	200	5.5	
8-H1	hhpsi84s13fp02	kinneret	dt	34	23	19	52	-12.00				R
9-A2	hhpsi84s17rp01	kinneret	dt	46	81	65	67	13.39	30	410	3.9	
10-B2	hhpsi84sesrp04	kinneret	dt	45	56	53	75	13.08	30	410	2.4	
11-C2	bsnme29s27rp01	kinneret	dt	43	35	21	43	-12.00				R
12-D2	hsnme29s27fp02	kinneret	dt									N
13-E2	HCACI93RP20	FISCHER	6815	88	61	66	35	13.43	20	380	4.5	
14-F2	HCACI93FP23	FISCHER	6816	53	116	221	76	13.61	30	410	4.4	
15-G2	HCACI93FP21	FISCHER	6817									N
16-H2	HCACI93FP22	FISCHER	6818									N
17-A3	HIBEC52RP20	FISCHER	6815	46	91	103	73	12.67	30	380	3.2	
18-B3	HIBEC52FP23	FISCHER	6816	29	72	121	63	13.41	20	280	5.4	
19-C3	HIBEC52FP21	FISCHER	6817	32	33	14	37	-12.00				R
20-D3	HIBEC52FP22	FISCHER	6818									N
21-E3	HAEAX59RP01	rad/kincaid	10007	26	30	13	37	-12.00				R
22-F3	HOSBQ35RP01	rad/kincaid	10005									N
23-G3	hhpsh35s14fp15	t curtis	6825	35	54	39	53	12.96	40	250	5.6	
24-H3	hhpsh35s14fp16	t curtis	6826	27	52	54	57	13.11	50	180	5.6	
25-A4	pgmdt	control	dt	613	370	212	203	13.76	60	350	1	
26-B4	HIBEC5250 1 FP	FISCHER		214	129	53	72	13.83	50	350	2	
27-C4	HIBEC52504 FP	FISCHER		202	198	53	50	13.83	50	345	1	
28-D4	HIBEC52501 FQ	FISCHER		281	165	55	87	13.82	50	345	4	
29-E4	HIBEC52504 FQ	FISCHER		230	195	45	69	13.91	50	350	0	
30-F4	m.mr	control	ppR	490	292	251	154	13.90	83	330	1	
31-G4	HTCD25R	RPW		256	238	137	99	14.01	92	320	0	
32-H4	HNE1421Rb	HLA		183	117	81	63	13.75				R

RETRACKED: SRK

Analyzed by: _SRK + Ivy_   Factura/Blast Analysis: _____

Uploaded by: _Ivy_   Folder: _Full Length + Scientists_

Primer 029
Pgem 040

Lor A4 C019
A4 C018

52

HTPANO8.

PQE60.
　5'NCO　1955.　Start

GTA	GCA	CCA	TGG	GAG	GAC	AAG	TAC	TCC

　5'Nco　251　Start.

GTA	CGA	CCA	TGG	ATk	ACG	AAG	GAG	AGT

　3'Bam HI　Stop.

AGA	TCG	GAT.CCC	AAC	TAA	AAA	GGC	CCC

PD10.
　5'Bam HI　Start　188
　　　ClGA

GTA	CGA	GGA	TCGGAGGA	GAA	GTA	CTC	CAA

　5'Bam HI　Start　251

GTA	CGA	GGA	TCC	AAT	GAC	GAA	GAG	AGT

　3'Hind III　Stop

CGC	GTA	AAGCTT	GGA	ACT	AAA	AAG	GCT

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Applied Biosystems

Synthesis Order - 2240 5' bam hi start 188

Run date: 7/19/94
Run ID: 2240 ak
Customer: ann kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 2240 5' bam hi start 188
Sequence: GTA CGA GGA TCC CAG GAC AAG TAC TCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-1" col 4 seq 34 at 7/19/94 12:13 PM.

Applied Biosystems

Synthesis Order - 2238 3' hind iii stop

Run date: 7/19/94
Run ID: 2238 ak
Customer: ann kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 2238 3' hind iii stop
Sequence: CGC GTA AAG CTT GGA ACT AAA AAG GCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
Sent to "Synthesizer-1" col 2 seq 32 at 7/19/94 12:12 PM.

Applied Biosystems

Synthesis Order - 2239 5'bam hi start 251

Run date: 7/19/94
Run ID: 2239 ak
Customer: ann kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 2239 5'bam hi start 251
Sequence: GTA CGA GGA TCC AAT GAC GAA GAG AGT

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

  Sent to "Synthesizer-1" col 3 seq 33 at 7/19/94 12:13 PM.

ob Applied Biosystems

Synthesis Order - 2241 3' bam hi stop

Run date: 7/19/94
Run ID: 2241
Customer: ann kim

1.   cx
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 3' bam hi stop
Sequence: AGA TCG GAT CCC AAC TAA AAA GGC CCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-2" col 3 seq 33 at 7/20/94 7:10 AM.

ab Applied Biosystems

Synthesis Order - 2243 5' nco start 185

Run date: 7/19/94
Run ID: 2243
Customer: ann kim

1.   cx
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 5'nco start 185
Sequence: GTA GCA CCA TGG GAG GAC AAG TAC TCC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-1" col 1 seq 31 at 7/20/94 11:40 AM.

Applied Biosystems

Synthesis Order - 2244 5' nco start 251

Run date: 7/19/94
Run ID: 2244
Customer: ann kim

1.   cx
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 5' nco start 251
Sequence: GTA CGA CCA TGG ATG ACG AAG GAG AGT

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-1" col 2 seq 32 at 7/20/94 11:41 AM.

Human Genome ~iences, Inc.   Plate I.D.(s ᵃ FOR 3_REDOS FROM 7/21/94

Date Initiated: 07/22/94   Results Folder: 04/23/94 SO HGS

Date Completed: 11/25/94   % Good: 7/2   % Good:

Templates	Sequence Reaction	Gel Run		
Method: MISC	Method: MANUAL/ BIOMEK	Machine ID:	SO	
Prep Person:	Prep Person: CDL	Gel Loader:	TA I	
Prep Date:	Prep Date: 07/22/94	Run Date:	7/22/94	

#	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trast SCode
1-A8	BLUESCRIPT	control	DP	487	356	154	143	11.83				M
2-B8	HPOAA6SF	NING	FOR	91	44	44	66	~12.16				R
3-C8	HTOEB44F	SUK	FOR	155	116	45	45	11.41	80	300	.3	
4-D9	HTOEB44AF	SUK	FOR	142	115	45	45	11.88	80	340	0	
5-E9	HTPANO8SO4Fb	A. KIM	FOR	109	399	103	98	11.98	80	270	3	
6-F9	HTPANO8ST3Fb	A. KIM	FOR	272	145	77	71	11.76	50	340	0	
7-G9	Test PGEMS 1	—	REV	3~2	343	100	114	11.74	40	360	7	
8-H9	2			349	233	145	91	11.58	40			M
9-A10	3			191	113	74	60	11.52	86	134	4	
10-B10	4			310	233	115	81	11.71	42	213	6	
11-C10	5			104	61	41	31	11.71	86	134	5	
12-D10	6			135	104	57	43	11.70	40	140	5	
13-E10												
14-F10												
15-G10												
16-H10												
17-A11												
18-B11												
19-C11												
20-D11												
21-E11												
22-F11												
23-G11												
24-H11												
25-A12												
26-B12												
27-C12												
28-D12												
29-E12												
30-F12												
31-G12												
32-H12												

Analyzed by: THL   Factura/Blast Analysis:

loaded by: ✓   Folder: Till Lincoln, Scient. sl

Additional Comments: in conput!

- Very small primer piaks
- Gel image looks good

60

Date Initiated: 07/21/94

Date Completed: 7/23/94

Results Folder: 7/23/94 V. HGS

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method: MISC	Method: BIOMEK/manual	Machine ID: 40
Prep Person: MISC	Prep Person: CDL	Gel Loader: CSH Babu
Prep Date: MISC	Prep Date: 07/22/94	Run Date: 7/22/94

| # | Sample Name | Scientist name/init. control | Primer DP/DT | \multicolumn{4}{c}{Signal Strength} | Base Spacing | vector | Edited length | % N's | Trash Code |
				C	A	G	T					
1-A1	BLUESCRIPT	control	DP	202	36	103	97	10.07	90	410	3%	
2-B1	HPOAA6SR	NING	REV	27	29	23	17	-12.0				
3-C1	HTOEX74R	NING	REV	35	42	29	21	9.40				B
4-D1	HTPAN08S04Rb	A. KIM	REV	83	62	39	31	9.91	100	460	3%	L
5-E1	HTPAN08ST3Rb	A. KIM	REV	69	49	36	33	10.08	100	350	4%	
6-F1	HTOEB44R	SUK	REV	78	56	34	30	10.10	100	340	1%	
7-G1	HTOEB44AR	SUK	REV	80	58	39	37	10.12	100	370	1%	
8-H1	8413E1R	KINNERE	REV	101	47	46	35	9.43				L
9-A2	8413C11R	KINNERE	REV	81	67	48	31	10.06	90	410	3%	
10-B2	8413E2R	KINNERE	REV	76	30	24	22	9.38	100	320	2%	
11-C2	8413E3R	KINNERE	REV	44	45	37	24	9.24				L
.-D2	8413C12R	KINNERE	REV	44	32	24	11	9.95	100			L
13-E2	8413C1R	KINNERE	REV	69	58	37	26	10.0	100	400	2%	
14-F2	8413E4R	KINNERE	REV	56	51	33	18	9.95	100	370	2%	
15-G2	8413C13R	KINNERE	REV	107	49	40	36	9.93	100	290	1%	
16-H2	8413C2R	KINNERE	REV	94	76	48	40	9.99	100	320	2%	
17-A3	8413C14R	KINNERE	REV	46	35	30	23	9.31	170	130	1%	
18-B3	8413C3R	KINNERE	REV	50	54	40	29	9.97	100	350	1%	
19-C3	8413ESR	KINNERE	REV	86	71	49	28	9.99	100	390	3%	
20-D3	8413E6R	KINNERE	REV	57	43	40	25	9.25	180	130	2%	
21-E3	8413E7R	KINNERE	REV									
22-F3	8413E8R	KINNERE	REV	39	35	27	19	9.23	180	310	1%	N
23-G3	8413C4R	KINNERE	REV	74	52	37	28	9.99	100	280	2%	
24-H3	FB3B1R	LAURIE	REV	28	27	21	17	9.49				B
25-A4	FB17B1R	LAURIE	REV									N
26-B4	FB16C1R	LAURIE	REV									N
27-C4	FB17A1R	LAURIE	REV									N
28-D4	FB18A1R	LAURIE	REV	35	35	29	19	-12.0				B/L
29-E4	FB3C1R	LAURIE	REV	24	22	21	20	9.82				B/L
30-F4	FB16A1R	LAURIE	REV									N
31-G4	FB1C1R	LAURIE	REV	37	37	35	30	9.99	90			B
32-H4	FB19C1R	LAURIE	REV	29	24	24	22	9.87	90			R
				42	34	40	24	-12.0				R

Analyzed by: CDL

Factura/Blast Analysis: _____

Uploaded by: CDL   Folder: sci seq + fini length

Additional Comments: —Very small primer peaks

61

Applied Biosystems
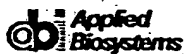
Synthesis Order - 7405 HTPAN08RP20

Run date: 7/25/94
Run ID: 7405 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7405 HTPAN08RP20 1280S
Sequence: GTG TAT CAC AGT AGT AGC CTC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-2" col 2 seq 32 at 7/26/94 7:44 AM.

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ab *Applied*
ab *Biosystems*

Synthesis Order - 7406 HTPANO8RP19

Run date: 7/25/94
Run ID: 7406 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7406 HTPANO8RP19   1031S
Sequence: GCA ATC TGA GTA GAG CAG C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-2" col 3 seq 33 at 7/26/94 7:45 AM.

63

ab Applied
ab Biosystems

Synthesis Order - 7407 HTPANO8FP18

Run date: 7/25/94
Run ID: 7407 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7407 HTPANO8FP18   756A
Sequence: GGA ATA GAG TCC ATA TTC TGC

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
  Sent to "Synthesizer-2" col 4 seq 34 at 7/26/94 7:46 AM.

64

Applied Biosystems

Synthesis Order - 7408 HTPAN08FP17

Run date: 7/25/94
Run ID: 7408 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 7408 HTPAN08FP17   561A
Sequence: GAC CAG TTC ACC ATT CCT C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-1" col 1 seq 31 at 7/26/94 7:48 AM.

65

Applied Biosystems

Synthesis Order - 7409 HTPANO8FP16

Run date: 7/25/94
Run ID: 7409 ak
Customer: Ann Kim

1.   jpw
2.
Synthesizer: Synthesizer-1
Model: 394-08
ROM version: 2.00

Sequence name: 7409 HTPANO8FP16   254A
Sequence: CAT ACT CTC TTC GTC ATT GG

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-1" col 2 seq 32 at 7/26/94 7:49 AM.

Human Genome Sciences, Inc.　　　Plate ...).(s) MISC. DT-2 _____

Date Initiated: 6/23/94 8/1/94 _____　　　Results Folder: 08/2/94 11 HGS

Date Completed: _____　　　% Good: 2/8 % Good: _____

	Templates		Sequence Reaction		Gel Run	
Method:			Method: MANUAL/BIOMEK		Machine ID: 11	
Prep Person:			Prep Person: JPF		Gel Loader: JPF	
Prep Date:			Prep Date: 8/1/94		Run Date: 8/1/94	

G A T C

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength G	A	T	C	Bases Spacing	Vector	Edited Length	% N's	Trash Code
1-A5	PGEM	control	DT	197	239	174	97	11.13	20	440	12%	
2-B5	hsnme29s14fp022	kinneret	7442									N
3-C5	hpfbq88testfp01	kinneret	7440	204	222	96	69	11.02	30	360	1%	
4-D5	HTPAN08SO4FP16	Ann Kim	7409	162	149	7 76	76	11.08	23	400	4%	
5-E5	HTPAN08SO4FP17	Ann Kim	7408	239	181	166	79	10.99	40	500	1%	
6-F5	HTPAN08SO4FP18	Ann Kim	7407	186	172	108	58	11.22	20	340	1%	
7-G5	HTPAN08SO4RP19	Ann Kim	7406	144	387	136	68	10.97	30	340	1%	
8-H5	HTPAN08SO4RP20	Ann Kim	7405	208	252	80	68	11.14	30	300	4%	
9-A6												
10-B6												
11-C6												
2-D6												
13-E6												
14-F6												
15-G6												
16-H6												
17-A7												
18-B7												
19-C7												
20-D7												
21-E7												
22-F7												
23-G7												
24-H7												
25-A8												
26-B8												
27-C8												
28-D8												
29-E8												
30-F8												
31-G8												
32-H8												

Analyzed by: _____　　　Factura/Blast Analysis: _____

Uploaded by: _____ Folder: Script/Full

Additional Comments:)

Human Genome Sciences, Inc.   Plate I.D.(s)   MISC DT_____ _____

Date Initiated: 6/29/94 _____   Results Folder: _08·03·94 11 HGS_

Date Completed: _08·03-94_____   % Good: _0/31_ = _1/290_ % Good: _25%_

Templates	Sequence Reaction	Gel Run
Method:MISC	Method:BIOMEK/MANUAL	Machine ID: 11
Prep Person:MISC	Prep Person: TES	Gel Loader: TB3
Prep Date:MISC	Prep Date:6/29/94 2'3	Run Date: 7.12

# / Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	Edited vector	length	% N	Trash Code
1-A1 PGEM	Control	DT	16	175	82	35	-12.00	10	280	6%	length
2-B1 HTPAN08S04RP01b	Ann Kim		213	759	117	80	-11.00	10	250	4%	
3-C1 HTPAN08S04RP03b	Ann Kim	5424	218	187	192	45	-12.00	10	340	5%	
4-D1 HTPAN08S04RP05b	Ann Kim	5426	28	494	211	67	-12.00	10	310	/	
5-E1 HTPAN08S04RP06b	Ann Kim	5676	132	580	200	78	-12.00	20	250	4%	
6-F1 HTPAN08S04RP07b	Ann Kim	5688	193	157	231	43	-12.00	50	300	3%	
7-G1 HTPAN08S04RP09b	Ann Kim	6422									N
8-H1 HTPAN08S04RP10b	Ann Kim	6445	117	184	91	50	-12.00	50	350	3%	
9-A2 HTPAN08S04RP12b	Ann Kim	6838	219	317	163	67	-11.00	10	390	2%	
10-B2 HTPAN08S04RP14b	Ann Kim	6640	302	207	200	92	-12.00	20	340	1%	
11-C2 HTPAN08S04FP15b	Ann Kim	6813	208	163	233	53	-12.00	40	310	/	
12-D2 HSUSH20DS01RP01	Ann Kim	6800									N
13-E2 HSUSH20DS01FP04	Ann Kim	6987									N
14-F2 HSUSH20DS02RP01	Ann Kim	6800									N
15-G2 HSUSH20DS02FP04	Ann Kim	6987									N
16-H2 HSUSH20DS03RP01	Ann Kim	6800									N
17-A3 HSUSH20DS03FP04	Ann Kim	6987									N
18-B3 HSUSH20DS04RP01	Ann Kim	6800									N
19-C3 HSUSH20DS04FP04b	Ann Kim	6987									N
20-D3 HSUSH20SO5RP01b	Ann Kim	6800									N
21-E3 HSUSH20SO5FP04	Ann Kim	6987									N
22-F3 HSUSH20DS06RP01	Ann Kim	6800									N
23-G3 HSUSH20DS06FP04	Ann Kim	6987									N
24-H3 HE20142DS01RP01	Ann Kim	6802									N
25-A4 HE20142DS01FP03 *	Ann Kim	6986									N
26-B4 HE20142DS01RP05	Ann Kim	7027									N
27-C4 HE20142DS02RP01	Ann Kim	6802									N
28-D4 HE20142DS01FP03+ SO3.01	Ann Kim	6986									N
29-E4 HE20142DS02RP05	Ann Kim	7027									N
30-F4 HIBEB69RP01	Ann Kim	7437	126	107	66	64	-12.00	10	440	1%	
31-G4 HIBEB69FP02	Ann Kim	7436									N
32-H4 HPDOM93RP01	Ann Kim	7439	61	43	49	19	-11.00	10	200	3%	enough

Analyzed by: _CY8_   Factura/Blast Analysis: _____

Uploaded by: _LX8_   Folder: _Sintists Full Length_

Additional Comments:

Gel B

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Human Genome Sciences, Inc.

Plate I.D.(s) _Manual DPs 1_

Date Initiated: 08/02/94

Date Completed: _08/03/94_

Results Folder: _08/03/94 30 HGS_

% Good: _8/33_ % Good: _25%_

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: _30_
Prep Person:	Prep Person: ROX	Gel Loader: _ROX_
Prep Date:	Prep Date: 08/02/94	Run Date: _08/03/94_

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% N=	Trash Code
1-A1	BLUESCRIPT REV	control	ReV	405	263	159	120	10.54	104	200	39%	
2-b1	VEG53-HE92	Laurie		13	16	56	48	10.28	97			P
3-C1	HTPAND5S04R1	Ann Kim		114	67	74	65	10.53	96			R
4-D1	HE8BP35S55	Laurie/AK		171	74	75	33	-1200				P
5-E1	HCEOJ49R	soppet/g		59	46	25	25	10.27	107	190	20%	
6-F1	HHFBK43R	soppet/g		68	34	43	20	-1200				P
7-G1	HPRAE77R	soppet/g		132	161	51	52	10.38	98	144	10%	
8-H1	HTEAL83Rc	Kunsch										N
9-A2	HIBEH64S1R	Bednarik		281	214	82	84	10.61	91	224	10%	
10-B2	HIBEH64S2R	Bednarik		258	149	71	71	10.67	94	228	2%	
11-C2	HIBEH64S3R	Bednarik		331	224	149	113	10.19	94	156	20%	
12-D2	HIBEH64S4R	Bednarik		82	65	31	31	10.50	92	200	2%	
13-E2	HIBEH64S5R	Bednarik										N
14-F2	HIBEH64S6R	Bednarik		324	149	53	72	10.60	91	185	10%	
15-G2	HE8BP35S01	GAH		249	80	90	67	10.7				R
16-H2	HE8BP35S05	GAH		202	74	92	68	-1200				P
17-A3	HE8BP35S06	GAH		140	60	63	39	10.48				R
18-B3	HE8BP35S07	GAH		142	59	61	45	10.73				R
19-C3	HE8BP35S08	GAH		25	102	92	104	-1200				P
20-D3	HE8BP35S10	GAH		146	54	56	31	10.71				R
21-E3	HE8BP35S13	GAH		204	63	84	65	10.81				R
22-F3	HE8BP35S39	GAH		195	61	62	61	-1200				P
23-G3	HE8BP35S40	GAH		186	73	74	61	-1200				P
24-H3	HE8BP35S43	GAH		209	79	65	48	10.93				R
25-A4	HE8BP35S44	GAH		203	73	76	56	10.77				R
26-B4	HE8BP35S45	GAH		20	31	37	29	.065				R
27-C4	HE8BP35S46	GAH		134	49	61	44	10.87				R
28-D4	HE8BP35S48	GAH		140	52	59	46	10.90				R
29-E4	HE8BP35S50	GAH		34	31	38	29	-1200				P
30-F4	HE8BP35S52	GAH		79	35	53	38	10.61				R
31-G4	HE8BP35S53	GAH		78	33	52	33	10.91				P
32-H4	HE8BP35S54	GAH		51	20	34	25	10.10				P

Analyzed by: _ROX_

Uploaded by: _ROX_ Folder: _Sciena Full_

Factura/Blast Analysis: _____

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Human Genome Sciences, Inc.

Plate I.D.(s) _Manual DPs 2_

Templates	Sequence Reaction	Gel Run
Method:	Method: Mr 7 o!	Machine ID: 37
Prep Person:	Prep Person: +C·X	Gel Loader: ROX
Prep Date:	Prep Date: 08/02/94	Run Date: 08/02/94

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	% vector	Edited length	% N's	Trash Code
1-A5	BLUESCRIPT FOR	CON	FoR	1008	70	37	28	11.53	10	319	19%	
2-B5	HCEOJ49F	soppet/g	/	65	70	38	31	11.25	67	280	0%	
3-C5	HHFBK43F	soppet/g	/	105	61	57	166	−1200	21	?		D
4-D5	HPRAE77F	soppet/g	/	32	17	71	49	11.31	81	225	1%	
5-E5	HTPAN08S04Fc	Ann Kim/		36	39	108	69	11.30	63	246	19%	
6-F5	HIBEH64S1F	Bednarik		32	216	9	70	11.31	64	263	19%	
7-G5	HIBEH64S2F	Bednarik		573	396	173	133	11.31	61	295	19%	
8-H5	HIBEH64S3F	Bednarik		250	163	86	85	11.33	65	277	19%	
9-A6	HIBEH64S4F	Bednarik		301	195	114	67	11.35	66	271	19%	
10-B6	HIBEH64S5F	Bednarik		301	145	114	67	11.37	66	258	19%	
11-C6	HIBEH64S6F	Bednarik		346	244	121	98	11.38	66	257	19%	
2-D6	HiBEB69Fba	Am Kim		314	177	123	71	11.25				R
13-E6	HTc3H42Faa	Jian N.		369	281	131	106	11.34	62	234	19%	
14-F6	H3vATS1Faa	Jian N.	✓	512	266	154	100	11.19	14	300	<10%	
15-G6	HMSB259Faa	Jian N.	FcR	716	482	278	162	11.23	61	271	<10%	
16-H6	Bluscript R	control	Rev	48	25	18	78	11.35	101	220	2%	
17-A7	H3vATS1Raa	Jian N.		108	704	29	230	11.30	100	234	09%	
18-B7	HMSB259Raa	Jian N.		116	30	46	35	11.17				R
19-C7	HIBEC52GSilRa	Fischer		526	259	134	97	11.12	109	190	30%	
20-D7	HIBEC52GSi2Ra	Fischer		120	53	85	92	−1200				R
21-E7	HIBEC52GS23Ra	D. Kozak		228	163	73	45	11.14	109	214	09%	
22-F7	HIBEC52GS24Ra	D. Kozak										N
23-G7	HE29D40ARa	D. Kozak		171	131	58	38	11.10	109	189	<19%	
24-H7	HE29D40B2a	D. Kozak										N
25-A8	LAP34RAa	JPW		63	56	33	28	10.69				R
26-B8	LAP34RBa	JPW										N
27-C8	LAP34RCa	JPW	✓									N
28-D8	HE3MZ50Raa	Brent	Rev	276	49	29	187	−12.00				R
29-E8	Mug's Bluescript F test	control	FoR	303	186	83	92	11.13	110	347	00%	
30-F8												
31-G8												
32-H8												

analyzed by: ROX

Uploaded by: ROX   Folder: Scien& Full L

Factura/Blast Analysis: _____

Additional Comments:

70

Query= HTPAN08XX
       (1643 letters)

Translating both strands of query sequence in all 6 reading frames

Database: nr
          125,275 sequences; 35,024,229 total letters.
Searching...done

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Smallest Poisson Probability P(N)	N
pir|S|A40201	artifact-warning sequence (trans...	+2	241	4.2e-71	3
pir|S|C40201	artifact-warning sequence (trans...	+1	246	2.3e-58	2
pir|S|F40201	artifact-warning sequence (trans...	+2	180	5.5e-21	2
gp|X55777|HSMHCHHS_2	H.sapiens Mahlavu hepatocellular...	+2	190	7.0e-21	1
pir|S|D40201	artifact-warning sequence (trans...	+2	81	2.3e-18	4
gp|L27065|HUMNF2A_1	NF2 gene product [Homo sapiens]	-3	139	1.1e-13	1
pir|S|E40201	artifact-warning sequence (trans...	+1	98	2.5e-13	3
gp|L20321|HUMSTK2A_1	protein serine/threonine kinase ...	-1	137	4.8e-12	1
gp|S58722|S58722_1	X-linked retinopathy protein (3'...	-1	128	1.9e-11	1
pir|S|A46010	X-linked retinopathy protein (C-...	-1	128	1.9e-11	1
gp|M84237|HUMIGTB1A_2	integrin beta-1 subunit [Homo sa...	-3	116	2.5e-10	1
pir|S|A42442	beta 1 integrin subunit, beta 1S...	-3	116	2.5e-10	1
gp|L24521|HUMTRRP_1	transformation-related protein [...	-3	120	2.5e-09	1
gp|U06948|MMU06948_1	Fas ligand [Mus musculus]	+1	84	3.7e-09	2
gp|L11672|HUMKRUPZN_1	zinc finger protein [Homo sapien...	+3	108	1.5e-07	1
gp|U03470|RNU03470_1	ligand for Fas antigen [Rattus n...	+1	84	2.1e-07	2
gp|L26953|HUMPROTXA_1	Homo sapiens chromosomal protein...	+2	101	1.1e-06	1
gp|X14828|CHTNFA_1	Goat mRNA for tumour necrosis fa...	+1	65	6.8e-06	2
pir|S|S06192	tumor necrosis factor alpha prec...	+1	65	6.8e-06	2
gp|A06305|A06305_1	lymphotoxin [None]	+1	99	1.2e-05	1
pir|S|B26359	decay-accelerating factor 2 prec...	-3	96	1.2e-05	1
pir|S|B32877	tumor necrosis factor beta precu...	+1	99	1.4e-05	1
pir|S|S34742	lymphotoxin - human	+1	99	1.4e-05	1
pir|S|S26951	tumor necrosis factor beta - human	+1	99	1.4e-05	1
gp|A00324|A00324_1	tumor necrosis factor beta [Arti...	+1	99	1.4e-05	1
gp|A06316|A06316_1	lymphotoxin [Homo sapiens] >gp|D...	+1	99	1.6e-05	1
gp|D00102|HUMLTX_1	Human lymphotoxin (LT) mRNA, com...	+1	99	1.6e-05	1
gp|Z15026|HSTNFABX_2	lymphotoxin, Tnfb gene product [...	+1	99	1.6e-05	1
gp|X77317|CHTNFAMR_1	tumour necrosis factor alpha [Ca...	+1	63	1.9e-05	2
gp|X55966|OATNFA_1	tumor necrosis factor alpha [Ovi...	+1	67	3.5e-05	2
gp|X55152|OATNFA1_1	tumor necrosis factor alpha (cac...	+1	67	3.5e-05	2
gp|X54859|SSTNFAB_1	Tumour necrosis factor beta [Sus...	+1	95	6.2e-05	1
gp|Z14137|BTTNFG_2	tumor necrosis factor alpha [Bos...	+1	65	6.9e-05	2
gp|M12845|RABTNFM_1	Rabbit tumor necrosis factor (TN...	+1	66	7.0e-05	2
gp|M60340|RABTNFB_2	tumor necrosis factor [Oryctolag...	+1	66	7.0e-05	2
gp|M55913|HUMTNFBA_1	tumor necrosis factor-beta [Homo...	+1	93	0.00012	1
pir|S|A26359	decay-accelerating factor 1 prec...	-3	89	0.00015	1
gp|X14800|MMTNFB_3	Murine mRNA 3'-fragment for tumo...	+1	92	0.00015	1
gp|X14800|MMTNFB_1	Murine mRNA 3'-fragment for tumo...	+1	92	0.00017	1
gp|M16819|MUSTNFBA_1	Mouse tumor necrosis factor-beta...	+1	92	0.00017	1

WARNING: Descriptions of 164 database sequences were not reported due to the
         limiting value of parameter V = 40.

71

>gp|U06948|MMU06948_1 fas ligand [Mus musculus]
          Length = 279

  Plus Strand HSPs:

 Score = 84 (40.2 bits), Expect = 0.0029, P = 0.0029
 Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 529 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 630
              G + +S +   + G LVI+E G Y++YS+ YFR Q
Sbjct: 165 GTALISGVKYKKGGLVINETGLYFVYSKVYFRGQ 198

 Score = 76 (36.4 bits), Expect = 3.7e-09, Poisson P(2) = 3.7e-09
 Identities = 16/77 (20%), Positives = 36/77 (46%), Frame = +1

Query: 655 NDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 834
              N++ + +Y S   L++ + +   + +S Y G +F L   D ++V+++
Sbjct: 201 NNQPLNHKVYMRNSKYPEDLVLMEEKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNIS 260

Query: 835 NEHLIDMDHEASFFGAF 885
              LI+ +   +FFG +
Sbjct: 261 QLSLINFEESKTFFGLY 277

 Score = 40 (19.1 bits), Expect = 0.84, Poisson P(3) = 0.57
 Identities = 6/13 (46%), Positives = 9/13 (69%), Frame = +1

Query: 259 EESMNSPCWQVKW 297
              ++ MN PC Q+ W
Sbjct: 2 QQPMNYPCPQIFW 14

>gp|L11672|HUMKRUPZN_1 zinc finger protein [Homo sapiens] >pir|S|S35305 finger
          protein ZNF91 – human
          Length = 1191

  Plus Strand HSPs:

 Score = 108 (54.9 bits), Expect = 1.5e-07, P = 1.5e-07
 Identities = 20/37 (54%), Positives = 26/37 (70%), Frame = +3

Query: 1371 VQWLTPVIPTFWEPKVGRSRDQEIKTIVTNIVKPHLY 1481
              + +TPVIP WE + G SR QE++TI+ N VKP LY
Sbjct: 1155 IHTITPVIPLLWEAEAGGSRGQEMETILANTVKPLLY 1191

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
          Length = 278

  Plus Strand HSPs:

 Score = 84 (40.2 bits), Expect = 0.0029, P = 0.0029
 Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 529 GHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 630
              G + +S +   + G LVI+E G Y++YS+ YFR Q
Sbjct: 164 GTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ 197

 Score = 70 (33.5 bits), Expect = 2.1e-07, Poisson P(2) = 2.1e-07
 Identities = 12/39 (30%), Positives = 23/39 (58%), Frame = +1

Query: 769 YSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 885
              +S Y G +F L   D ++V+++   LI+ +   +FFG +
Sbjct: 238 HSSYLGAVFNLTVADHLYVNISQLSLINFEESKTFFGLY 276

EDITED 08/08/94.CON.SEQ Map (1 > 1643)Site and Sequence
Enzymes :   All 417 enzymes (No Filter)
Settings :   Circular, Certain Sites Only, Standard Genetic Code

```
GGCACGAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATGATGGAGGTCC
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+ 70
CCGTGCTCGCCGACGGACCGACTGAATGTCGTCAGTCTGAGACTGTCCAAGTACCGATACTACCTCCAGG

   G  T  S  G  C  L  A  D  L  Q  Q  S  Q  S  D  R  F  M  A  M  M  E  V
    A  R  A  A  A  W  L  T  Y  S  S  Q  T  L  T  G  S  W  L  .  W  R  S
   R  H  E  R  L  P  G  .  L  T  A  V  R  L  .  Q  V  H  G  Y  D  G  G  P
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
   P  V  L  P  Q  R  A  S  K  C  C  D  S  E  S  L  N  M  A  I  I  S  T  W
    A  R  A  A  A  Q  S  V  .  L  L  .  V  R  V  P  E  H  S  H  H  L  D
     C  S  R  S  G  P  Q  S  V  A  T  L  S  Q  C  T  .  P  .  S  P  P  G

AGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGTGCTCCTGCAGTCTCTCTG
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+ 140
TCCCCCCTGGGTCGGACCCTGTCTGGACGCACGACTAGCACTAGAAGTGTCACGAGGACGTCAGAGAGAC

   Q  G  G  P  S  L  G  Q  T  C  V  L  I  V  I  F  T  V  L  L  Q  S  L  C
    R  G  D  P  A  W  D  R  P  A  C  .  S  .  S  S  Q  C  S  C  S  L  S
     G  G  T  Q  P  G  T  D  L  R  A  D  R  D  L  H  S  A  P  A  V  S  L
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
   P  P  G  L  R  P  C  V  Q  T  S  I  T  I  K  V  T  S  R  C  D  R  Q
    L  P  S  G  A  Q  S  L  G  A  H  Q  D  H  D  E  C  H  E  Q  L  R  E  T
     P  P  V  W  G  P  V  S  R  R  A  S  R  S  R  .  L  A  G  A  T  E  R

TGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGC
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+ 210
ACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTCGTCTACGTCCTGTTCATGAGGTTTTCACCG

   V  A  V  T  Y  V  Y  F  T  N  E  L  K  Q  M  Q  D  K  Y  S  K  S  G
    V  W  L  .  L  T  C  T  L  P  T  S  .  S  R  C  R  T  S  T  P  K  V  A
     C  G  C  N  L  R  V  L  Y  Q  R  A  E  A  D  A  G  Q  V  L  Q  K  W
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
   T  A  T  V  .  T  Y  K  V  L  S  S  F  C  I  C  S  L  Y  E  L  L  P
    H  S  Y  S  V  H  V  K  G  V  L  Q  L  L  H  L  V  L  V  G  F  T  A
     H  P  Q  L  K  R  T  S  .  W  R  A  S  A  S  A  P  C  T  S  W  F  H  C

ATTGCTTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCT
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+ 280
TAACGAACAAAGAATTTTCTTCTACTGTCAATAACCCTGGGGTTACTGCTTCTCTCATACTTGTCGGGGA

   I  A  C  F  L  K  E  D  D  S  Y  W  D  P  N  D  E  E  E  S  M  N  S  P
    L  L  V  S  .  K  K  M  T  V  I  G  T  P  M  T  K  R  V  .  T  A  P
     H  C  L  F  L  K  R  R  .  Q  L  L  G  P  Q  .  R  R  E  Y  E  Q  P  L
+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
   M  A  Q  K  K  F  S  S  S  L  .  Q  S  G  L  S  S  S  L  I  F  L  G  Q
    N  S  T  E  .  F  F  I  V  T  I  P  V  G  I  V  F  L  T  H  V  A  G
     Q  K  N  R  L  L  L  H  C  N  N  P  G  W  H  R  L  S  Y  S  C  G  R
```

73

```
GCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCAT
----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 350
CGACCGTTCAGTTCACCGTTGAGGCAGTCGAGCAATCTTTCTACTAAAACTCTTGGAGACTCCTTTGGTA
```

```
   C  W  Q  V  K  W  Q  L  R  Q  L  V  R  K  M  I  L  R  T  S  E  E  T  I
    A  G  K  S  S  G  N  S  V  S  S  L  E  R  .  F  .  E  P  L  R  K  P
       L  A  S  Q  V  A  T  P  S  A  R  .  K  D  D  F  E  N  L  .  G  N  H
```

```
----+----+----+----+----+----+----+----+----+----+----+----+----+----+
    Q  C  T  L  H  C  S  R  .  S  T  L  F  I  I  K  L  V  E  S  S  V  M
     A  P  L  D  L  P  L  E  T  L  E  N  S  L  H  N  Q  S  G  R  L  F  G  N
       S  A  L  .  T  A  V  G  D  A  R  .  F  S  S  K  S  F  R  Q  P  F  W
```

```
TTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 420
AAGATGTCAAGTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTTCTCCAGGAGTCTCTCATCGT
```

```
    S  T  V  Q  E  K  Q  Q  N  I  S  P  L  V  R  E  R  G  P  Q  R  V  A
   F  L  Q  F  K  K  S  N  K  I  F  L  P  .  E  K  E  V  L  R  E  .  Q
    F  Y  S  S  R  K  A  T  K  Y  F  S  P  S  E  R  K  R  S  S  E  S  S
```

```
----+----+----+----+----+----+----+----+----+----+----+----+----+----+
    E  V  T  .  S  F  C  C  F  I  E  G  R  T  L  S  L  P  G  .  L  T  A
   R  C  N  L  F  L  L  L  I  N  R  G  .  H  S  F  S  T  R  L  S  Y  C
    K  .  L  E  L  F  A  V  F  Y  K  E  G  L  S  L  F  L  D  E  S  L  L  L
```

```
GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAATGAAAAGGCTC
----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 490
CGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTGAGGTTCTTACTTTTCCGAG
```

```
   A  H  I  T  G  T  R  G  R  S  N  T  L  S  S  P  N  S  K  N  E  K  A
    L  T  .  L  G  P  E  E  E  A  T  H  C  L  L  Q  T  P  R  M  K  R  L
  S  S  H  N  W  D  Q  R  K  K  Q  H  I  V  F  S  K  L  Q  E  .  K  G  S
```

```
----+----+----+----+----+----+----+----+----+----+----+----+----+----+
   A  .  M  V  P  V  L  P  L  L  L  V  N  D  E  G  F  E  L  F  S  F  A  R
    S  V  Y  S  P  G  S  S  S  A  V  C  Q  R  R  W  V  G  L  I  F  L  S
     E  C  L  Q  S  W  L  F  F  C  C  M  T  K  E  L  S  W  S  H  F  P  E
```

```
TGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTCCTGAGCAACTTGCACTTGAG
----+----+----+----+----+----+----+----+----+----+----+----+----+----+ 560
ACCCGGCGTTTTATTTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAGGACTCGTTGAACGTGAACTC
```

```
   L  G  R  K  I  N  S  W  E  S  S  R  S  G  H  S  F  L  S  N  L  H  L  R
    W  A  A  K  .  T  P  G  N  H  Q  G  V  G  I  H  S  .  A  T  C  T  .
     G  P  Q  N  K  L  L  G  I  I  K  E  W  A  F  I  P  E  Q  L  A  L  E
```

```
       P  R  L  I  F  E  Q  S  D  D  L  L  P  C  E  N  R  L  L  K  C  K  L
      Q  A  A  F  Y  V  G  P  F  .  .  P  T  P  M  .  E  Q  A  V  Q  V  Q  P
        P  G  C  F  L  S  R  P  I  M  L  S  H  A  N  M  G  S  C  S  A  S  S
```

```
GAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 630
CTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATGTAGATAAGGGTTTGTATGAAAGCTAAAGTC

    N  G  E  L  V  I  H  E  K  G  F  Y  Y  I  Y  S  Q  F  F  F  R  F  Q
    G  M  V  N  W  S  S  M  K  K  G  F  T  T  S  I  P  K  H  T  F  D  F  R
    E  W  .  T  G  H  P  .  K  R  V  L  L  H  L  F  P  N  I  L  S  I  S
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
    F  P  S  S  T  M  W  S  F  P  N  .  .  M  .  E  W  V  Y  K  R  N  .
     I  T  F  Q  D  D  M  F  F  P  K  V  V  D  I  G  L  C  V  K  S  K  L
    S  H  H  V  P  .  G  H  F  L  T  K  S  C  R  N  G  F  M  S  E  I  E  P


GAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 700
CTCCTTTATTTTCTTTTGTGTTTCTTGCTGTTTGTTTACCAGGTTATATAAATGTTTATGTGTTCAATAG

    E  E  I  K  E  N  T  K  N  D  K  Q  M  V  Q  Y  I  Y  K  Y  T  S  Y
    R  K  .  K  K  T  Q  R  T  T  N  K  W  S  N  I  F  T  N  Q  V  I
    G  G  N  K  R  K  H  K  E  R  Q  T  N  G  P  I  Y  L  Q  I  H  K  L  S
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
    S  S  I  F  S  F  V  F  F  S  L  C  I  T  W  Y  I  .  L  Y  V  L  .  G
    L  F  Y  F  F  V  C  L  V  V  F  L  H  D  L  I  N  V  F  V  C  T  I
     P  F  L  L  F  C  L  S  R  C  V  F  P  G  I  Y  K  C  I  C  L  N  D


CTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 770
GACTGGGATATAACAACTACTTTTCACGATCTTTATCAACAACCAGATTTCTACGTCTTATACCTGAGAT

    P  D  P  I  L  L  M  K  S  A  R  N  S  C  W  S  K  D  A  E  Y  G  L  V
    L  T  L  Y  C  .  .  K  V  L  E  I  V  V  G  L  K  M  Q  N  M  D  S
     .  P  Y  I  V  D  E  K  C  .  K  .  L  L  V  .  R  C  R  I  W  T  L
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
     S  G  I  N  N  I  F  L  A  L  F  L  Q  Q  D  L  S  A  S  Y  P  S  .
    R  V  R  Y  Q  Q  H  F  T  S  S  I  T  T  P  R  F  I  C  F  I  S  E  I
    Q  G  .  I  T  S  S  F  H  .  F  Y  N  N  T  .  L  H  L  I  H  V  R


TTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+ 840
AAGGTAGATAGTTCCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC

    S  I  Y  Q  G  G  I  F  E  L  K  E  N  D  R  I  F  V  S  V  N  E
    T  P  S  I  K  G  E  Y  L  S  L  R  K  M  T  E  F  L  F  L  .  Q  M  S
    F  H  L  S  R  G  N  I  .  A  .  G  K  .  Q  N  F  C  F  C  N  K  .
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
    E  M  .  .  P  P  I  N  S  S  L  S  F  S  L  I  K  T  E  T  V  F  S
     G  D  I  L  P  S  Y  K  L  K  L  F  I  V  S  N  K  N  R  Y  C  I  L
    N  W  R  D  L  P  F  I  Q  A  .  P  F  H  C  F  K  Q  K  Q  L  L  H  A
```

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EDITED 08/08/94.CON.SEQ Map (1 > 1643)Site and Sequence

```
CACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTTAGTTGGCTAACTGACCTGGAAAG
+--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--+ 910
GTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAACCGATTGACTGGACCTTTC

 H  L  I  D  M  D  H  E  A  S  F  F  G  A  F  L  V  G  .  L  T  W  K
    T  .  T  W  T  M  K  P  V  F  S  G  P  F  .  L  A  N  .  P  G  K
 A  L  D  R  H  G  P  .  S  Q  F  F  R  G  L  F  S  W  L  T  D  L  E  R

 C  K  I  S  M  S  W  S  A  L  K  K  P  A  K  K  T  P  .  S  V  Q  F  S
    V  Q  Y  V  H  V  M  F  G  T  K  E  P  G  K  .  N  A  L  Q  G  P  F
    S  S  L  C  P  G  H  L  W  N  K  R  P  R  K  L  Q  S  V  S  R  S  L


AAAAAGCAATAACCTCAAAGTGACTATTCAGTTTTCAGGATGATACACTATGAAGATGTTTCAAAAAATC
+--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--+ 980
TTTTTCGTTATTGGAGTTTCACTGATAAGTCAAAAGTCCTACTATGTGATACTTCTACAAAGTTTTTTAG

 E  K  A  I  T  S  K  .  L  F  S  F  Q  D  D  T  L  .  R  C  F  K  K  S
    K  K  Q  .  P  Q  S  D  Y  S  V  F  R  M  I  H  Y  E  D  V  S  K  N
    K  S  N  N  L  K  V  T  I  Q  F  S  G  .  Y  T  M  K  M  F  Q  K  I

    F  A  I  V  E  F  H  S  N  L  K  .  S  S  V  S  H  L  H  K  L  F  D
 F  F  C  Y  G  .  L  S  .  E  T  K  L  I  I  C  .  S  S  T  E  F  F  R
    F  L  L  L  R  L  T  V  I  .  N  E  P  H  Y  V  I  F  I  N  .  F  I


TGACCAAAACAAACAAACAGAAAACAGAAAACAAAAAAACCTCTATGCAATCTGAGTAGAGCAGCCACAA
+--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--+ 1050
ACTGGTTTTGTTTGTTTGTCTTTTGTCTTTTGTTTTTTTGGAGATACGTTAGACTCATCTCGTCGGTGTT

 D  Q  N  K  Q  T  E  N  R  K  Q  K  N  L  Y  A  I  .  V  E  Q  P  Q
 L  T  K  T  N  K  Q  K  T  E  N  K  K  T  S  M  Q  S  E  .  S  S  H  N
 .  P  K  Q  T  N  R  K  Q  K  T  K  K  P  L  C  N  L  S  R  A  A  T

 S  W  F  L  C  V  S  F  L  F  C  F  F  R  .  A  I  Q  T  S  C  G  C
    V  L  V  F  L  C  F  V  S  F  L  F  V  E  I  C  D  S  Y  L  L  W  L
    Q  G  F  C  V  F  L  F  C  F  V  F  F  G  R  H  L  R  L  L  A  A  V  V


CCAAAAAATTCTACAACACACACTGTTCTGAAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAA
+--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--I--+--+--+--+ 1120
GGTTTTTTAAGATGTTGTGTGTGACAAGACTTTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTT

 P  K  N  S  T  T  H  T  V  L  K  V  T  H  L  S  Q  E  N  E  I  A  E
    Q  K  I  L  Q  H  T  L  F  .  K  .  L  T  Y  P  K  K  M  K  L  L  K
 T  K  K  F  Y  N  T  H  C  S  E  S  D  S  L  I  P  R  K  .  N  C  .  K

 G  F  F  E  V  V  C  V  T  R  F  T  V  .  K  D  W  S  F  S  I  A  S  L
 W  F  I  R  C  C  V  S  N  Q  F  H  S  V  .  G  L  F  I  F  N  S  F
    L  F  N  .  L  V  C  Q  E  S  L  S  E  S  I  G  L  F  H  F  Q  Q  F
```

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```
GATCTTTCAGGACTCTACCTCATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATT
----+----|----+----|----+----|----+----|----+----|----+----|----+----+ 1190
CTAGAAAGTCCTGAGATGGAGTATAGTCAAACGATCGTCTTTAGATCTTCTGACAGTCGAAGGTTTGTAA

   R  S  F  R  T  L  P  H  I  S  L  L  A  E  I  .  K  T  V  S  F  Q  T  L
    D  L  S  G  L  Y  L  I  S  V  C  .  Q  K  S  R  R  L  S  A  S  K  H
     I  F  Q  D  S  T  S  Y  Q  F  A  S  R  N  L  E  D  C  Q  L  P  N  I
----+----|----+----|----+----|----+----|----+----|----+----|----+----+
     D  K  L  V  R  G  .  I  L  K  S  A  S  I  .  F  V  T  L  K  W  V  N
    S  R  E  P  S  .  R  M  D  T  Q  .  C  F  D  L  L  S  D  A  E  L  C  .
     I  K  .  S  E  V  E  Y  .  N  A  L  L  F  R  S  S  Q  .  S  G  F  M

AATGCAATGGTTAACATCTTCTGTCTTTATAATCTACTCCTTGTAAAGACTGTAGAAGAAAGCGCAACAA
----+----|----+----|----+----|----+----|----+----|----+----|----+----+ 1260
TTACGTTACCAATTGTAGAAGACAGAAATATTAGATGAGGAACATTTCTGACATCTTCTTTCGCGTTGTT

   M  Q  W  L  T  S  S  V  F  I  I  Y  S  L  .  R  L  .  K  K  A  Q  Q
    .  C  N  G  .  H  L  L  S  L  .  S  T  P  C  K  D  C  R  R  K  R  N  N
     N  A  M  V  N  I  F  C  L  Y  N  L  L  L  V  K  T  V  E  E  S  A  T
----+----|----+----|----+----|----+----|----+----|----+----|----+----+
     I  C  H  N  V  D  E  T  K  I  I  .  E  K  Y  L  S  Y  F  F  A  C  C
      H  L  P  .  C  R  R  D  K  Y  D  V  G  Q  L  S  Q  L  L  F  R  L  L
    L  A  I  T  L  M  K  Q  R  .  L  R  S  R  T  F  V  T  S  S  L  A  V  I

TCCATCTCTCAAGTAGTGTATCACAGTAGTAGCCTCCAGGTTTCCTTAAGGGACAACATCCTTAAGTCAA
----+----|----+----|----+----|----+----|----+----|----+----|----+----+ 1330
AGGTAGAGAGTTCATCACATAGTGTCATCATCGGAGGTCCAAAGGAATTCCCTGTTGTAGGAATTCAGTT

   S  I  S  Q  V  V  Y  H  S  S  S  L  Q  V  S  L  R  D  N  I  L  K  S
    P  S  L  K  .  C  I  T  V  V  A  S  R  F  P  .  G  T  T  S  L  S  Q
   I  H  L  S  S  S  V  S  Q  .  .  P  P  G  F  L  K  G  Q  H  P  .  V  K
----+----|----+----|----+----|----+----|----+----|----+----|----+----+
   D  M  E  .  T  T  Y  .  L  L  L  R  W  T  E  K  L  S  L  M  R  L  D  F
    G  D  R  L  Y  H  I  V  T  T  A  E  L  N  G  .  P  V  V  D  K  L  .
     W  R  E  L  L  T  D  C  Y  Y  G  G  P  K  R  L  P  C  C  G  .  T  L

AAGAGAGAAGAGGCACCACTAAAAGATCGCAGTTTGCCTGGTGCAGTGGCTCACACCTGTAATCCCAACA
----+----|----+----|----+----|----+----|----+----|----+----|----+----+ 1400
TTCTCTCTTCTCCGTGGTGATTTTCTAGCGTCAAACGGACCACGTCACCGAGTGTGGACATTAGGGTTGT

   K  E  R  R  G  T  T  K  R  S  Q  F  A  W  C  S  G  S  H  L  .  S  Q  H
    K  R  E  E  A  P  L  K  D  R  S  L  P  G  A  V  A  H  T  C  N  P  N
     R  E  K  R  H  H  .  K  I  A  V  C  L  V  Q  W  L  T  P  V  I  P  T
----+----|----+----|----+----|----+----|----+----|----+----|----+----+
    S  L  L  P  V  V  L  L  D  C  N  A  Q  H  L  P  E  C  R  Y  D  W  C
   F  L  S  S  A  G  S  F  S  R  L  K  G  P  A  T  A  .  V  Q  L  G  L  M
    L  S  F  L  C  W  .  F  I  A  T  Q  R  T  C  H  S  V  G  T  I  G  V
```

```
TTTTGGGAACCCAAGGTGGGTAGATCACGAGATCAAGAGATCAAGACCATAGTGACCAACATAGTGAAAC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  1470
AAAACCCTTGGGTTCCACCCATCTAGTGCTCTAGTTCTCTAGTTCTGGTATCACTGGTTGTATCACTTTG

   F  G  N  P  R  W  V  D  H  E  I  K  R  S  R  P  .  .  P  T  .  .  N
  I  L  G  T  Q  G  G  .  I  T  R  S  R  D  Q  D  H  S  D  Q  H  S  E  T
  F  W  E  P  K  V  G  R  S  R  D  Q  E  I  K  T  I  V  T  N  I  V  K
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
  K  P  F  G  L  H  T  S  .  S  I  L  L  D  L  G  Y  H  G  V  Y  H  F
   K  P  V  W  P  P  Y  I  V  L  D  L  S  .  S  W  L  S  W  C  L  S  V
  N  Q  S  G  L  T  P  L  D  R  S  .  S  I  L  V  M  T  V  L  M  T  F  G

CCCATCTCTACTGAAAGTGCAAAAATTAGCTGGGTGTGTTGGCACATGCCTGTAGTCCCAGCTACTTGAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  1540
GGGTAGAGATGACTTTCACGTTTTTAATCGACCCACACAACCGTGTACGGACATCAGGGTCGATGAACTC

   P  I  S  T  E  S  A  K  I  S  W  V  C  W  H  M  P  V  V  P  A  T  .
   P  S  L  L  K  V  Q  K  L  A  G  C  V  G  T  C  L  .  S  Q  L  L  E
   P  H  L  Y  .  K  C  K  N  .  L  G  V  L  A  H  A  C  S  P  S  Y  L  R
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
  G  M  E  V  S  L  A  F  I  L  Q  T  H  Q  C  M  G  T  T  G  A  V  Q  S
   G  D  R  S  F  T  C  F  N  A  P  H  T  P  V  H  R  Y  D  W  S  S  S
    W  R  .  Q  F  H  L  F  .  S  P  T  N  A  C  A  Q  L  G  L  .  K  L

AGGCTGAGGCAGGAGAATCGTTTGAACCCGGGAGGCAGAGGTTGCAGTGTGGTGAGATCATGCCACTACA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  1610
TCCGACTCCGTCCTCTTAGCAAACTTGGGCCCTCCGTCTCCAACGTCACACCACTCTAGTACGGTGATGT

  E  A  E  A  G  E  S  F  E  P  G  R  Q  R  L  Q  C  G  E  I  M  P  L  H
   R  L  R  Q  E  N  R  L  N  P  G  G  R  G  C  S  V  V  R  S  C  H  Y
    G  .  G  R  R  I  V  .  T  R  E  A  E  V  A  V  W  .  D  H  A  T  T
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
   A  S  A  P  S  D  N  S  G  P  L  C  L  N  C  H  P  S  I  M  G  S  C
  L  S  L  C  S  F  R  K  F  G  P  P  L  P  Q  L  T  T  L  D  H  W  .  V
   P  Q  P  L  L  I  T  Q  V  R  S  A  S  T  A  T  H  H  S  .  A  V  V

CTCCAGCCTGGCGACAGAGCGAGACTTGGTTTC
+---+---+---+---+---+---+--->  1643
GAGGTCGGACCGCTGTCTCGCTCTGAACCAAAG

   S  S  L  A  T  E  R  D  L  V  S
  T  P  A  W  R  Q  S  E  T  W  F
   L  Q  P  G  D  R  A  R  L  G  F
+---+---+---+---+---+---+---+-->
   E  L  R  A  V  S  R  S  K  T  L
    G  A  Q  R  C  L  S  V  Q  N  A
  S  W  G  P  S  L  A  L  S  P  K
```

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Alignment Report of Untitled, using Clustal method with PAM250 residue weight table.
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```
              10              20              30
      M - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVE091.pep
      M - - - - - - - - - - - - - - - - - - - - - S T E S M I R   TNFa.pep
  1   M - - - - - - - - - - - - - - - - - - - - - T P P E R L F   TNFb
  1   M G A - - - - - - - - - - - - - - - - - - - - - - - - - L   LTb
  1   M Q Q P V N Y P C P Q I Y W V D S S A T S P W A P P G S V F   FASL.pep


              40              50              60
  2   - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVE091.pep
  9   D V E L A E E - - - - - - - - - - - - - - - - - - - - - -   TNFa.pep
  9   - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
  5   G L E G R G G R L Q G R - - - - - - - - - G S L L L A V A G   LTb
 31   S C P S S G P R G P G Q R R P P P P P P P P S P L P P P S Q   FASL.pep


              70              80              90
  2   - - - - - - - - - - - R R F L S - K V Y S F P M - - -       HUVE091.pep
 16   - - A L P K K T G G P Q G S R R C L F L S L F S F L I V A G  TNFa.pep
  9   - - - L P R V C G T T - - - - - L H L L L G L L L V - -     TNFb
 26   A T S L V T L - - - - - - - - - L L A V P I T V L A V L A    LTb
 61   P P P L P P L S P L K K K D N I E L W L P V I F F M V L V A  FASL.pep


              100             110             120
 14   - - - R K L I L F L V F P V - - - V - - - - - - - - - -     HUVE091.pep
 44   - - A T T L F C L L H F G V - - - I G P Q R E E S P R D L S  TNFa.pep
 28   - - - - - - - - - L L - - - - - - - P G A Q G L P - G V G   TNFb
 46   L V P Q D Q G - - - - - G L V T E T A D P G A Q A Q Q G L G  LTb
      L V G M G L G M Y Q L F H L Q K E L A E L R E F T N H S L R  FASL.pep


              130             140             150
 26   - - - - - - - - R Q T P T Q H F K N Q F - - - - - - - -     HUVE091.pep
 69   L I S P L A Q A V R S S S R T - - - P S D K P V A H V V A   TNFa.pep
 40   L T P S A A Q T A R Q H P K M H L A H S T L K P A A H L I G  TNFb
 71   F - - - - Q K L P E E E P E T D L S P G L - - P A A H L I G  LTb
121   V S S F E K Q I A N P S T P S E T K K P - - R S V A H L T G  FASL.pep


              160             170             180
 38   - - - - - P - A L H W E H E L G L A F T K N R M N Y T N - K  HUVE091.pep
 95   N P Q A E G - Q L Q W L N R R A N A L L A N G V E L R D - N  TNFa.pep
 70   D P S K Q N - S L L W R A N T D R A F L Q D G F S L S N - N  TNFb
 95   A P L K - G Q G L G W E T T K E Q A F L T S G T Q F S D A E  LTb
149   N P R S R S I P E E W D T Y G T A L I - S G V K Y K K - G    FASL.pep


              190             200             210
 61   F L L I P E S G D F I Y S Q V T F R G M T S E C S E I R Q    HUVE091.pep
123   Q E V V P S E G L L I Y S Q V L F K G Q G C - - - - - - -   TNFa.pep
 98   S L L V P T S G I Y F V Y S Q V V F S G K A Y S P K A - - -  TNFb
124   G E A L P Q D G L Y Y L Y C L V G Y R G R A P P G G G D P Q  LTb
177   G L V I N E A G L Y F V Y S K V Y F R G Q S C N S Q P - - -  FASL.pep
```

...nment Report of Untitled, using Clustal method with PAM250 residue weight table.

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```
                  220             230             240
      A G R P N K P D S I T V V I T K V T D S Y P E P T Q - - E L   HUVEO91.pep
 _+6  - - - P S T H V L L T H T I S R I A V S Y Q T K V N - - L L   TNFa.pep
 125  - - - P S S P L Y L A H E V Q L F S S Q Y P F H V P - - E D   TNFb
 154  G - - - - R S V T L R S S L Y R A G G A Y G P G T P E L L E   LTb
 204  - - - - - - - L S H K V Y M R N F K W P G D L V - - L M       FASL.pep


                  250             260             270
 119  M G T K S V C E - - - - - - - - V G S N W F Q P I Y L G A     HUVEO91.pep
 171  S A I K S P C Q R E T P E G - A E A K P W Y E P I Y L G G     TNFa.pep
 150  S S Q K M V Y P - - - - - - - G L Q E P W L H S M Y H G A     TNFb
 180  E G A E T V T P V L D P A R R Q G Y G P L W Y T S V G F G G   LTb
 223  E E K K L N Y - - - - - C - - T T G Q I W A H S S Y L G A     FASL.pep


                  280             290             300
 140  M F S L Q E G D K L M V N V S D I S L V D Y T K E D K T P Y   HUVEO91.pep
 199  V F Q L E K G D R L S A E I N R P D Y L D F A E S G Q V Y F   TNFa.pep
 172  A F Q L T Q G D Q L S T H T D G I P H L V L S - P S T V F F   TNFb
 210  L V Q L R R G E R V Y V N I S H P D M V D F A R - G K T F F   LTb
 245  V F N L T V A D H L Y V N I S Q L S L I N F - E E S K T F F   FASL.pep


 170  G A F L L                                     HUVEO91.pep
 229  G I I A L                                     TNFa.pep
 201  G A F A L                                     TNFb
 239  G A V M V G                                   LTb
  '4  G L Y K L                                     FASL.pep
```

Decoration 'Decoration #1': Box residues that match the Consensus within 2 distance units.

```
LOCUS           CHTNFAMR_1
DEFINITION      C.hircus TNF-alpha mRNA. Tumour necrosis factor alpha; NCBI
                gi: 452608.
DATE            01-FEB-1994
ACCESSION       X77317
ORGANISM        Capra hircus Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . .


to: U06948.Gp_All   check: 3291   from: 1  to: 279

LOCUS           MMU06948_1
DEFINITION      Mus musculus Fas ligand mRNA, complete cds. NCBI gi: 473565.
DATE            29-APR-1994
ACCESSION       U06948
ORGANISM        Mus musculus Eucaryotae; Metazoa; Chordata; Vertebrata;
                Gnathostomata; Mammalia; Eutheria; Rodentia; Myomorpha; Muridae; . .


Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
CompCheck: 1254

        Gap Weight:   3.000     Average Match:   0.540
     Length Weight:   0.100     Average Mismatch: -0.396

          Quality:   82.2           Length:    160
            Ratio:   0.548            Gaps:      5
Percent Similarity: 48.993   Percent Identity: 29.530

X77317.Gp_All x U06948.Gp_All August 9, 1994  17:02  ..


   1 QTLSSSSQASSNKPVAHVVANI.SAPGQLRWGDSYANALKANGVALKDNQ 49
     .. |..|: ... :.|||:.:|   |  . .| |:|.|:.|| :|| .|...
 130 ANPSTPSEKKEPRSVAHLTGNPHSRSIPLEWEDTYGTAL.ISGVKYKKGG 178

  50 LVVPNDGLYLIYSQVLFRGHGCPSTPLFLTQTISRIAVSDQTKVNILSAI 99
     ||: :.|||::||.|.|||::|  .  |   |.:.: . . . ...: ::..
 179 LVINETGLYFVYSKVYFRGQSCNNQP..LNHKVYMRNSKYPEDLVLMEEK 226

 100 KSPCHRETPEGAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPEYLDYAES 149
     : : :      ...:. |  .. | |:||.|..:|:|  .:|.  ..::.||
 227 RLNY......CTTGQIWAHSSYLGAVFNLTSADHLYVNISQLSLINFEES 270

 150 GQVYFGIIAL 159
     ..:||:. |
 271 .KTFFGLYKL 279
$
```

```
LOCUS       MMU06948_1
DEFINITION  Mus musculus Fas ligand mRNA, complete cds. NCBI gi: 473565.
DATE        29-APR-1994
ACCESSION   U06948
ORGANISM    Mus musculus Eucaryotae; Metazoa; Chordata; Vertebrata;
            Gnathostomata; Mammalia; Eutheria; Rodentia; Myomorpha; Muridae; . .


to: X55152.Gp_All  check: 8990  from: 1  to: 234

LOCUS       OATNFA1_1
DEFINITION  O.aries mRNA for tumor necrosis factor alpha (TNF-alpha).
            Tumor necrosis factor alpha (cachetin); NCBI gi: 1406.
DATE        09-APR-1992
ACCESSION   X55152
ORGANISM    Ovis aries Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . . .


Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
CompCheck: 1254
```

	Gap Weight:	3.000	Average Match:	0.540
	Length Weight:	0.100	Average Mismatch:	-0.396

	Quality:	109.8	Length:	275
	Ratio:	0.473	Gaps:	10
Percent	Similarity:	49.321	Percent Identity:	28.054

```
U06948.Gp_All x X55152.Gp_All August 9, 1994  17:03  ..


 16 DSSATSSWAPPGSVFPCPSCGPRGPDQRRPPPPPPPVSPLPPPSQPLPLP  65
    ..| ... . ::.|:. ...||.|.    :.
  3 TKSMIRDVELAEEVLSNKAGGPQGSRSCWC...................  32

 66 PLTPLKKKDHNTNLWLPVVFFMVLVALVGMGLGMYQLFHLQKELAELREF 115
              |.:. |:      ||: : .:: |:|:. ::.. ||
 33 ...............LSLFSFL....LVAGATTLFCLLHFG.VIGPQRE.  61

116 TNQSLKVSSFEKQIANP.STPSEKKEPRSVAHLTGNPHSRSIPLEWEDTY 164
    :|| ..||::.:... ...|: .: :.|||:.:| | . :| |:|.|
 62 .EQSPAGPSFNRPLVQTLRSSSQASNNKPVAHVVANI.SAPGQLRWGDSY 109

165 GTALIS.GVKYKKGGLVINETGLYFVYSKVYFRGQSCNNQP..LNHKVYM 211
    :.||:. ||..|...||: ..|||::||.|.|||::| . | |.|.:. .
110 ANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISR 159

212 RNSKYPEDLVLMEEKRLNY......CTTGQIWAHSSYLGAVFNLTSADHL 255
    . .|...: ::.. :  :      ....:. | .. | |:||.|:..:|:|
160 IAVSYQTKVNILSAIKSPCHRETLEGAEAKPWYEPIYQGGVFQLEKGDRL 209

256 YVNISQLSLINFEES.KTFFGLYKL 279
    .:|.  ..::::.|| ..:||:. |
210 SAEINLPEYLDYAESGQVYFGIIAL 234
```

     9 LQQSDSDRFMAMMEVQGGPSLG..........QTCVLIVIFTVLLQSLCV 48
       :: |....: : .| ..|| | .... : :.. |.|.:
    15 VDSSATSSWAPPGSVFPCPSCGPRGPDQRRPPPPPPPVSPLPPPSQPLPL 64

    49 AVTYVYFTNELKQMQDKYSRSGIACFLKEDDSYWDPNDEESMNSPCWQVK 98
       :.   :| |. ::. . .:. |:   . :|. . :|:
    65 PP....LTPLKKKDHNTNLNLPVVFFMVLV.......ALVGMGLGMYQLF 103

    99 WQLRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRG 148
       ::|. . : . . .:|..:.. .| |.   .::|..|│///////::
   104 HLQKELAELREFTNQSLKVSSFEKQIANPSTPSEKKEPRSVAHLTGNPHS 153

   149 RSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGF 198
       || .|...:. | .::|.:..:.|:|||:|.|:
   154 RSIPLEWEDT.................YGTALISGVKYKKGQLVINETGL 186

   199 YYIYSQTYFRFQEEIKENTKNDKQMVQYLYKYTS.YPDPILLMKSARNSC 247
       |::||..||| :.. |:..: : :||. .| ||:.::||.. |′.:
   187 YFVYSKVYFR......GQSCNNQPLNHKVYMRNSKYPEDLVLMEEKRLNY 230

   248 WSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 297
       ..:. :: .| | |::|:|...|:::|.:.. ||::::.. .||| : :
   231 CTTGQIWA.HSSYLGAVFNLTSADHLYVNISQLSLINFEESKTFFGLYKL 279

$

TRANSLATE of: htpan08xx.dat check: 8776 from: 1 to: 1643
generated symbols 1 to: 547.
 REFORMAT of: Htpan08xx.Dat check: -1 from: 1 to: 1643 August 9, 1994 15:18
 (No documentation)

 to: X55152.Gp_All check: 8990 from: 1 to: 234

LOCUS   OATNFA1_1
DEFINITION O.aries mRNA for tumor necrosis factor alpha (TNF-alpha).
            Tumor necrosis factor alpha (cachetin); NCBI gi: 1406.
DATE   09-APR-1992
ACCESSION   X55152
ORGANISM   Ovis aries Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . . .

 Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
 CompCheck: 1254

           Gap Weight: 3.000   Average Match: 0.540
        Length Weight: 0.100   Average Mismatch: -0.396

              Quality: 93.8   Length: 299
                Ratio: 0.404   Gaps: 9
  Percent Similarity: 47.391   Percent Identity: 22.174

 Htpan08xx.Pep x X55152.Gp_All August 9, 1994 15:36 ..

    1 GTSGCLADLQQSDSDRFMAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAV 50
      :l.: : l:: .:.   .: : .lll :..l : :l..ll :..l.
    2 STKSMIRDVELAEE....VLSNKAGGPQGSRSCWCLSLFSFLL..VAGAT 45

   51 TYVYFTNELKQMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQ 100
      l..:: :   :: l   ...:l:l .:l::.
   46 TLFCLLH........FGVIG...........PQREEQSPAGPSFN.... 71

  101 LRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRS 150
      l.ll. .ll.l.:.   : .:..ll:.:. : .
   72 .RPLVQ..TLRSSSQA................SNNKPVAHVVANISAP 100

  151 NTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYY 200
      . l...:l ..: ::   ...:.l::.:ll:...l:l.
  101 GQLRWGDSYANALMA...............NGVELKDNQLVVPTDGLYL 134

  201 IYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSK 250
      llll..ll :: _.   .. : .. .l .. .: : :ll: :.
  135 IYSQVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETLE 184

  251 DAEYGLY..SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 297
      :ll   : .llll:l:l...ll: ..:. ....:l ...: .: ::::.
  185 GAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPEYLDYAESGQVYFGIIA 233

TRANSLATE of: htpan08xx.dat check: 8776 from: 1 to: 1643
generated symbols 1 to: 547.
 REFORMAT of: Htpan08xx.Dat check: -1 from: 1 to: 1643 August 9, 1994 15:18
 (No documentation)

 to: X77317.Gp_All check: 8996 from: 1 to: 159

LOCUS   CHTNFAMR_1
DEFINITION C.hircus TNF-alpha mRNA. Tumour necrosis factor alpha; NCBI
            gi: 452608.
DATE   01-FEB-1994
ACCESSION   X77317
ORGANISM   Capra hircus Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; . .

Symbol comparison table: Gencoredisk:[Gcgcore.Data.Rundata]Swgappep.Cmp
CompCheck: 1254

        Gap Weight: 3.000   Average Match: 0.540
     Length Weight: 0.100   Average Mismatch: -0.396

           Quality: 68.5   Length: 166
             Ratio: 0.466   Gaps: 5
Percent Similarity: 47.482   Percent Identity: 25.899

Htpan08xx.Pep x X77317.Gp_All August 9, 1994 15:37 ..

    151 NTL.SSPNSKNEKALGRKINSWESS...RSGHSFLSNLH.....LRNGEL 191
        .II II.....:I:::: :.. .... I.I.I: ..I.   I::.:I
      1 QTLSSSSQASSNKPVAHVVANISAPGQLRWGDSYANALKANGVALKDNQL 50

    192 VIHEKGFYYIYSQTYFR..........FQEEIKENTKNDKQMVQYIYKYT 231
        I:..:.I:I.IIII..II   : :.I. . .I. .I..: ..
     51 VVPNDGLYLIYSQVLFRGHGCPSTPLFLTQTISRIAVSDQTKVNILSAIK 100

    232 SYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEH 281
        I   .: I:.. : :I. . .IIIII:I:I...II: ...:. ..
    101 S........PCHRETPEGAEAKPWYEPIYQGGVFQLEKGDRLSAEINLPE 142

    282 LIDMDHEASFFGAFLV 297
        .:I ....: .: :::.
    143 YLDYAESGQVYFGIIA 158

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National Center for Biotechnology Information (NCBI)

Experimental GENINFO(R) BLAST Network Service (Hgssun3)

Wed Aug 10 17:52:09 EDT 1994, Up 16 day(s), 1:44, load: 0.94, 2.16, 3.54

If results of this search are reported or published, please mention that
the computation was performed at the NCBI using the BLAST network service.
Problems with the service should be reported to a local system administrator.

Welcome to the HGS Network Blast Server!

Databases available on the HGS server:

name	description
hgs	HGS/TIGR ESTs human through 08/08/94
hgs_nh	HGS/TIGR non-human ESTs through 08/03/94
thc	TIGR Human Concensus Sequences through 08/08/94
hgs_new	Current Month's HGS/TIGR ESTs through 08/08/94
nt	Non-redundant nucleotide database as of 06/13/94
human-nt	Human sequences from nt database as of 06/13/94
human-est	Human EST sequences from nt database as of 06/13/94
nr	Non-redundant protein database as of 06/13/94
blocks	BLOCKS Motif database, version 7.01

Problems or questions, contact Mike Fannon. Have a BLAST!   -- MRF

BLASTN 1.3.12MP [29-Oct-93] [Build 12:00:00 Nov 11 1993]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers,
and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol.
215:403-410.

Notice: this program is optimized to find nearly identical sequences rapidly.
To identify weak similarities encoded in nucleic acid, use BLASTX or TBLASTN.

Query= HTTCI56R
        (477 letters, both strands)

Database: hgs
          283,367 sequences; 103,639,919 total letters.
Searching...done

	Sequences producing High-scoring Segment Pairs:	High Score	Smallest Poisson Probability P(N)	N
HTTCI56R	Unknown, Group 16833	2277	6.0e-185	1
HTPAN08S04R	Unknown, Group 16833	1437	6.5e-115	1
HTPAN08XX	Unknown, Group 16833	1204	3.1e-93	1
HTPAN08S04FP14	Unknown, Group 16833	1014	7.5e-80	1
HTPAN08S04RP12	Unknown, Group 16833	999	1.2e-78	1
HTPAN08S04RP10	Ligand for Fas antigen [Rattus norvegicus]	751	1.2e-54	1
HTJAEC01R	Unknown, Group 16833	629	2.0e-45	1
HETAQ48R	Unknown, Group 16833	640	5.1e-45	1
HT2SE96R	Unknown, Group 16833	116	0.997	1
HLHSM30R	Unknown Sequence	106	1.000000	1
HBNAZ93R	Human adipocyte lipid-binding protein, com...	102	1.000000	1
HPFCO32R	Unknown, Group 10416	99	1.000000	1
HFCAN81R	Unknown, Group 8856	98	1.000000	1
HE2DV72R	Unknown, Group 8856	98	1.000000	1
HE9CT60R	Unknown, Group 8856	98	1.000000	1

HE2PS38R	Unknown, Group 8856	98	1.000000	1
HOSBQ17R	Homo sapiens integral membrane protein, ca...	98	1.000000	1
HE2GB47R	Human calnexin mRNA, complete cds.	98	1.000000	1
HEBCI61R	PBluescript	97	1.000000	1
HE2AY46R	Unknown Sequence	97	1.000000	1
HLTBS32R	Unknown, Group 10589	96	1.000000	1
HE9MG79R	Unknown, Group 41162	96	1.000000	1
HCEOR80R	Unknown, Group 53138	96	1.000000	1
HTBAA86R	Unknown, Group 64	95	1.000000	1
HOSCM10R	Unknown, Group 25755	95	1.000000	1
HFKCA55R	Putative opioid receptor [Homo sapiens]	94	1.000000	1
HAPAU68R	D.discoideum protein-tyrosine kinase-2 (DP...	94	1.000000	1
HPBEJ50R	Unknown, Group 2196	94	1.000000	1
HPBEJ50F	Unknown, Group 2196	94	1.000000	1
HCETB74R	Hardy-Zuckermann 4 feline sarcoma virus (H...	94	1.000000	1
HMEAF90R	Unknown, Group 2196	94	1.000000	1
HE2ED89R	Unknown, Group 38458	93	1.000000	1
HBNAB87R	Unknown, Group 27194	92	1.000000	1
HEBBN20R	Unknown, Group 27194	92	1.000000	1
HLHDP75R	Human mRNA encoding phosphoglycerate kinase.	92	1.000000	1
HT3SF69R	Unknown Sequence	91	1.000000	1
HONAH21R	Unknown, Group 42018	90	1.000000	1
HEPAK86R	ORF [Homo sapiens]	89	1.000000	1
HT2SG40R	Unknown, Group 31877	89	1.000000	1
HE9CU60R	Unknown, Group 8856	89	1.000000	1
HFCAD78R	Unknown, Group 1611	88	1.000000	1
HOSBV50R	Human p62 mRNA, complete cds.	88	1.000000	1
HCEDR10R	Unknown, Group 26335	88	1.000000	1
HT4CL52R	Unknown, Group 49412	88	1.000000	1
HE9CQ82R	H.sapiens mRNA for type I collagen	88	1.000000	1
HE2CT57R	Unknown, Group 8856	87	1.000000	1
HE2AX81R	Unknown, Group 8856	87	1.000000	1
HAUAI83R	Unknown, Group 3372	87	1.000000	1
HCEBF39R	Unknown, Group 10589	87	1.000000	1
HUKAT59F	Unknown, Group 14193	87	1.000000	1

WARNING: Descriptions of 3356 database sequences were not reported due to the
limiting value of parameter V = 50.

>HTTCI56R   Unknown, Group 16833
          Length = 477

   Plus Strand HSPs:

   Score = 2277 (629.2 bits), Expect = 6.0e-185, P = 6.0e-185
   Identities = 465/477 (97%), Positives = 465/477 (97%), Strand = Plus

Query: 1 GGCACGAGGAAGGAAGGGCTTCAGTGACCGGCTGCCTGGCTGACTTACAGCAGTNAGACT 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct: 1 GGCACGAGGAAGGAAGGGCTTCAGTGACCGGCTGCCTGGCTGACTTACAGCAGTNAGACT 60

Query: 61 CTGACAGGATCATGGCTATNATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCG 120
             ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct: 61 CTGACAGGATCATGGCTATNATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCG 120

Query: 121 TGCTGATCGTNATCTTCACAGTGCTGCTGCAGTCTCTCTGTGTGTGGCTGTAACTTACGTGT 180
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121 TGCTGATCGTNATCTTCACAGTGCTGCTGCAGTCTCTCTGTGTGTGGCTGTAACTTACGTGT 180

Query: 181 ACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTT 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181 ACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTT 240

87

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Query:   252 GATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAGCCCCTGCTGGCAAGTC 311
             |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct:   233 GATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTC 292

Query:   312 AAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGACCTCTGAGGNAACCATT 371
             ||||||||| ||||||||| ||||||||||||||| || || ||||||||| |||||||
Sbjct:   293 AAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTGGAGAACCTCTGAGGAAACCATT 352

Query:   372 TTTACAGTTCAAGNAAGCAACAAATTTTTTCTCCCC 406
             | |||||||||| || | || |||| || || ||
Sbjct:   353 TCTACAGTTCAAGAAAAGCAACAAATTTTTTCTCC 387

 Score = 490 (135.4 bits), Expect = 9.0e-68, Poisson P(2) = 9.0e-68
 Identities = 102/107 (95%), Positives = 102/107 (95%), Strand = Plus

Query:    26 GACCGGCTGCCTGGCTGACTTACAGCAGTNAGACTCTGACAGGATCATGGCTATNATGGA 85
             || ||||||||||||||||||||||||||| |||||||||| |||||||||||| |||||
Sbjct:     6 GAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCATGGCTATGATGGA 65

Query:    86 GGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTNA 132
             |||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct:    66 GGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGA 112

 Score = 116 (32.1 bits), Expect = 4.3e-10, Poisson P(3) = 4.3e-10
 Identities = 28/34 (82%), Positives = 28/34 (82%), Strand = Plus

Query:   393 AAATTTTTCTCCCCTAGTGAGGGNAAGNGTTCTT 426
             || |||||||||||||||| | ||| | || |
Sbjct:   376 AATTTTTTCTCCCCTAGTGAGAGAAAGAGGTCCT 409


>HTPANO8S04FP14  Unknown, Group 16833
          Length = 432

  Minus Strand HSPs:

 Score = 1014 (280.2 bits), Expect = 7.5e-80, P = 7.5e-80
 Identities = 206/210 (98%), Positives = 206/210 (98%), Strand = Minus

Query:   313 TTGACTTGCCAGCAGGGGCTGTTCATACTCTCCTCGTCATTGGGGTCCCAATAACTGTCA 254
             | |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct:   223 TGGACTTGCCAGCAGGGGCTGTTCATACTCTCTTCGTCATTGGGGTCCCAATAACTGTCA 282

Query:   253 TCTTCTTTTAAGAAACAAGCAATGCCACTTTTGGAGTACTTGTCCTGCATCTGCTTCAGC 194
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   283 TCTTCTTTTAAGAAACAAGCAATGCCACTTTTGGAGTACTTGTCCTGCATCTGCTTCAGC 342

Query:   193 TCGTTGGTAAAGTACACGTAAGTTACAGCCACACAGAGAGACTGCAGCAGCACTGTGAAG 134
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct:   343 TCGTTGGTAAAGTACACGTAAGTTACAGCCACACAGAGAGACTGCAGGAGCACTGTGAAG 402

Query:   133 ATNACGATCAGCACGCAGGTCTGTCCCAGG 104
             || |||||||||||||||||||||||||||
Sbjct:   403 ATCACGATCAGCACGCAGGTCTGTCCCAGG 432

 Score = 318 (87.9 bits), Expect = 1.1e-39, Poisson P(2) = 1.1e-39
 Identities = 78/96 (81%), Positives = 78/96 (81%), Strand = Minus

Query:   406 GGGGAGAAAAATTTGTTGCTTNCTTGAACTGTAAAAATGGTTNCCTCAGAGGTCCTNAAA 347
             || || || || | || | |||||||||| |||||||| |||||| || |||
Sbjct:   129 GGAGAAATATTTTGTTGCTTTTCTTGAACTGTAGAAATGGTTTCCTCAGAGGTTCTCAAA 188

Query:   346 ACCATCTTTCTAACGAACTGACGGAATTGCCACTTG 311
             | |||||||||||||| |||||||| ||||||||||
Sbjct:   189 ATCATCTTTCTAACGAGCTGACGGAGTTGCCACTTG 224
```

88

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Query:   241 TCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAGCCCCT 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   241 TCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAGCCCCT 300

Query:   301 GCTGGCAAGTCAAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGACCTCTG 360
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct:   301 GCTGGCAAGTCAAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGACCTCTG 360

Query:   361 AGGNAACCATTTTTACAGTTCAAGNAAGCAACAAATTTTTCTCCCCTAGTGAGGGNAAGN 420
             |||| ||||||||||||||||||||| |||||||||||||||||||||||||||||| |||
Sbjct:   361 AGGNAACCATTTTTACAGTTCAAGNAAGCAACAAATTTTTCTCCCCTAGTGAGGGNAAGN 420

Query:   421 GTTCTTAGAGNGTAGGAATTCACNTAATTGGGGCCANGGAAGAAGCAACANATTGT 477
             |||||||||| |||||||||||| ||||||||||| |||||||||||||| |||||
Sbjct:   421 GTTCTTAGAGNGTAGGAATTCACNTAATTGGGGCCANGGAAGAAGCAACANATTGT 477


>HTPAN08S04R      Unknown, Group 16833
              Length = 325

  Plus Strand HSPs:

  Score = 1437 (397.1 bits), Expect = 6.5e-115, P = 6.5e-115
  Identities = 301/318 (94%), Positives = 301/318 (94%), Strand = Plus

Query:    56 AGACTCTGACAGGATCATGGCTATNATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGAC 115
             - ||| |||||||||| ||||||||||| |||||||||||||||||||||||||||||||||
Sbjct:     1 AGANTCTGACAGGTTCATGGCTATGATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGAC 60

Query:   116 CTGCGGTGCTGATCGTNATCTTCACAGTGCTGCTGCAGTCTCTCTGTGTGGCTGTAACTTA 175
             |||| ||||||||||| |||||||||||||||| |||||||||||| ||||||||||||||
Sbjct:    61 CTGCTTGCTGATCGTNATCTTCACAGTGCTCCTGCAGTCTCTCTNTGTGTGGCTGTAACTTA 120

Query:   176 CGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGC 235
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   121 CGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGC 180

Query:   236 TTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAGGAGAGTATGAACAG 295
             ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct:   181 TTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAAGAGAGTATGAACAG 240

Query:   296 CCCCTGCTGGCAAGTCAAGTGGCAATTCCGTCAGTTCGTTAGAAAGATGGTTTTNAGGAC 355
             ||||||||||||||||||||||||||| ||||||||| ||||||||||| |||| || ||
Sbjct:   241 CCCCTGCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAAC 300

Query:   356 CTCTGAGGNAACCATTTT 373
             ||||||||| || | |||
Sbjct:   301 CTCTGAGGGAAACCATTT 318


>HTPAN08XX       Unknown, Group 16833
              Length = 1648

  Plus Strand HSPs:

  Score = 1204 (332.7 bits), Expect = 3.1e-93, P = 3.1e-93
  Identities = 256/275 (93%), Positives = 256/275 (93%), Strand = Plus

Query:   132 ATCTTCACAGTGCTGCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAAC 191
             ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   113 ATCTTCACAGTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAAC 172

Query:   192 GAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAA 251
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct:   173 GAGCTGAAGCAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAA 232
```

```
                    10              20              30
      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVE091.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFa.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   LTb
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   FASL.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   FAS LIGAND  U06948.pep
  1   G T S G C L A D L Q Q S D S D R F M A M M E V Q G G P S L G   HTPAN08XX.SEQ.FULL.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA   M55913.pep


                    40              50              60
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   HUVE091.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   TNFa.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   TNFb
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   LTb
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   FASL.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   FAS LIGAND  U06948.pep
 31   Q T C V L I V I P T V L L Q S L C V A V T Y V Y F T N E L K   HTPAN08XX.SEQ.FULL.pep
  1   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - M   HUMAN TNF BETA   M55913.pep


                    70              80              90
  2   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVE091.pep
  2   S T E S M I R D V E L - - - - - - - - - - - - - - - - - - -   TNFa.pep
  2   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
  2   G A L - - - - - - - - - - - - - - - - - - - - - - - - - - -   LTb
  2   Q Q P V N Y P C P Q I - - - - - - - - - Y W V - - - - D S S   FASL.pep
  2   Q Q P M N Y P C P Q I - - - - - - - - - F W V - - - - D S S   FAS LIGAND  U06948.pep
  1   Q M Q D K Y S K S G I A C F L K E D D S Y W D P N D E E S M   HTPAN08XX.SEQ.FULL.pep
  2   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA   M55913.pep


                   100             110             120
  2   - - - - - - - - - - - - - - - - A E E A L P K K T G G P Q G S -   HUVE091.pep
 13   - - - - - - - - - - - - - - - - A E E A L P K K T G G P Q G S -   TNFa.pep
  2   - - - - - T P - - - - - - - P E R L F L P R V C G T T - - -   TNFb
  5   - - - - - - - - - - - - - - - - - - - G L E G R G   LTb
 19   A T S P W A P - - - - - - - P G S V F S C P S S G P R G P G   FASL.pep
 19   A T S S W A P - - - - - - - P G S V F P C P S C G P R G P D   FAS LIGAND  U06948.pep
 91   N S P C W Q V K W Q L R Q L V R K M I L R T S E E T I S T V   HTPAN08XX.SEQ.FULL.pep
  2   - - - - - T P - - - - - - - P E R L F L P R V C G T T - - -   HUMAN TNF BETA   M55913.pep


                   130             140             150
  2   - R R - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUVE091.pep
 28   - R R C - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFa.pep
 17   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
 11   G R - - - - - - - - - - - - - - - - L Q G - - - - -   LTb
 42   Q R R P P P P P P P S P L P P P S Q P P P L P P - - - - -   FASL.pep
 42   Q R R P P P P P P V S P L P P P S Q P L P L P P - - - - -   FAS LIGAND  U06948.pep
121   Q E K Q Q N I S P L V R E R G P Q R V A A H I T G T R G R S   HTPAN08XX.SEQ.FULL.pep
 17   - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA   M55913.pep
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Alignment Report of alignment, using Clustal method with PAM250 residue weight table.
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                 160           170           180
                  |             |             |
      - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
 31   - - - - - - - - - - - - - - - - - - - - - - -[L]  TNFa.pep
 17   - - - - - - - - - - - - - - - - - - - - - - - -   TNFb
 16   - - - - - - - - - - - - - R G S L L L A V A G A T S  LTb
 67   - - - - - - - - - - - - L S P L K K K D N - I E[L]  FASL.pep
 67   - - - - - - - - - - - - L T P L K K K D H N T N[L]  FAS LIGAND  U06948.pep
151   N T L S S P N S K N E K A L G R K I N S W E S S R S G H S F  HTPAN08XX.SEQ.FULL.pep
 17   - - - - - - - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA   M55913.pep

                 190           200           210
                  |             |             |
  4   F[L S]K V Y -[S]F P[M]- - - - R K[L I]L F[L]V - -[F]P]V - -  HUVEO91.pep
 32   F[L S]-[L]F -[S]F[L I]V]A G A T T[L]F C[L]L]H - -[F G]V - -  TNFa.pep
 17   -[L H]L L L L G]L[L L V L]- - - - - - - - - - - - -  TNFb
 29  [L]V T L L L]A V P I T V[L]A V[L A L]V P Q D Q - - G[G L]V T  LTb
 79   W[L]P V I F F M[V L]V A[L]V G[M G L G M Y]Q[L]- -[F]H]L Q K  FASL.pep
 80   W[L]P V V F F M[V L]V A[L]V G[M G L G M Y]Q[L]- -[F]H]L Q K  FAS LIGAND  U06948.pep
181  [L S N L H]L R N G E[L V]I H E K]G[F Y Y L Y]S Q T Y[F]R F Q E  HTPAN08XX.SEQ.FULL.pep
 17   -[L H]L L L L G]L[L L V L]- - - - - - - - - - - - -  HUMAN TNF BETA   M55913.pep

                 220           230           240
                  |             |             |
 25   - V - - -[R Q]T[P]T[Q]H F K N Q F P - - - - - - - - - - -  HUVEO91.pep
 56   - I[G]P Q[R E]E S P R D[L S]L I[S]P[L A Q]A V R S[S]S R T P  TNFa.pep
 29   -[L]P G[A]Q G[L P G]V[G L T]P[S A A Q T]A R Q[H P]K[M H L A]  TNFb
 57   E[T A D]P G A Q A Q]Q G[L]G F Q K L P E[E P]E[T D]L]S P[G]  LTb
107   E L A E[L R E]F T N H S L]R[V S S]F[E]K]Q I A N P S]T P S E  FASL.pep
108   E L A E[L R E]F T N Q S L]K[V S S]F[E]K]Q I A N P S]T P S E  FAS LIGAND  U06948.pep
 11  [E]I K[E]N T K N D K]Q]M V Q Y I Y K Y]T]S Y P D P I[L L M]K  HTPAN08XX.SEQ.FULL.pep
 29   -[L]P G[A]Q G[L P G]V[G L T]P[S A A Q T]A R Q[H P]K[M H L A]  HUMAN TNF BETA   M55913.pep

                 250           260           270
                  |             |             |
 39   - - - - - - - - - - - - - - - - - - - - - - - -   HUVEO91.pep
 85  [S]D - -[K]- - - - - - - - - - - - - - - - - - - -   TNFa.pep
 58   H[S]T L[K]- - - - - - - - - - - - - - - - - - - -   TNFb
 87   L - - - - - - - - - - - - - - - - - - - - - - -   LTb
137  [T]K K P[R]- - - - - - - - - - - - - - - - - - - -   FASL.pep
138   K K E P[R]- - - - - - - - - - - - - - - - - - - -   FAS LIGAND  U06948.pep
241  [S A]R N S C W S K D A E Y G L Y S I Y Q G G I F E L K E N D  HTPAN08XX.SEQ.FULL.pep
 58   H[S]T L[K]- - - - - - - - - - - - - - - - - - -   HUMAN TNF BETA   M55913.pep

                 280           290           300
                  |             |             |
 39   - - - - - - - - - - - - - - - - - - - - - -[A]H]W]  HUVEO91.pep
 88   - - - - -[P]V]A H]V]V A N P]Q A]E G]- - - - - -[Q]L]Q]W]  TNFa.pep
 63   - - - - -[P A A H L I G D P S K Q N]- - - - - -[S]L L]W]  TNFb
 88   - - - - -[P]A A H L I G A P[L K]-]G]- - - - - - Q[G]L]G]W]  LTb
142   - - - - - S V]A H L[T]G N P]R S R]S]- - - - - - I P]L]E]W]  FASL.pep
143   - - - - - S V]A H L[T]G N P]H S R]S]- - - - - - I P]L]E]W]  FAS LIGAND  U06948.pep
271   R I F V S V T]N]E]H L I[D M D H E A]S]F F G A F L V]G]L]T]W]  HTPAN08XX.SEQ.FULL.pep
 63   - - - - -[P A A H L I G D P S K Q N]- - - - - -[S]L L]W]  HUMAN TNF BETA   M55913.pep
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Alignment Report of alignment, using Clustal method with PAM250 residue weight table.
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                    310              320              330
  3  E H E L G L A - - - - F T K N R M N - Y T N K - F L L I P E   HUVE091.pep
105  L N R R A N A - - - - L L A N G V E - L R D N - Q L V V P S   TNFa.pep
 80  R A N T D R A - - - - F L Q D G F S - L S N N - S L L V P T   TNFb
105  E T T K E Q A - - - - F L T S G T Q - F S D A E G L A L P Q   LTb
160  E D T Y G T A - - - - - L I S G V K - Y K K G - G L V I N E   FASL.pep
161  E D T Y G T A - - - - - L I S G V K - Y K K G - G L V I N E   FAS LIGAND  U06948.pep
301  K E K A I T S K L F S F Q D D T L R C F K S D Q N K Q T E   HTPAN08XX.SEQ.FULL.pep
 80  R A N T D R A - - - - F L Q D G F S - L S N N - S L L V P T   HUMAN TNF BETA   M55913.pep

                    340              350              360
 67  S - - - - G D Y F I Y S Q V T F R G M T S E C - - - - S E I   HUVE091.pep
129  E - - - - G L Y L I Y S Q V L F K G Q - - G C - - - - - - -   TNFa.pep
104  S - - - - G I Y F V Y S Q V V F S G K A Y S - - - - - - - -   TNFb
130  D - - - - G L Y Y L Y C L V G Y R G R A P P G - - - - G G -   LTb
183  A - - - - G L Y F V Y S K V Y F R G Q S C N - - - - - - - -   FASL.pep
184  T - - - - G L Y F V Y S K V Y F R G Q S C N - - - - - - - -   FAS LIGAND  U06948.pep
331  N R K Q K N L Y A I V E Q P Q P K N S T H T V L K V T H L   HTPAN08XX.SEQ.FULL.pep
104  S - - - - G I Y F V Y S Q V V F S G K A Y S - - - - - - - -   HUMAN TNF BETA   M55913.pep

                    370              380              390
 89  R Q A G R P N K P D S - - I T V V I T K V T D S - - - - - -   HUVE091.pep
146  - - - - - - P S T H V L - - L T H T I S R I A V S - - - - - -   TNFa.pep
122  - - P K A P S S P L Y - - L A H E V Q L F S S Q - - - - - -   TNFb
151  - - - D P Q G R S V T - - L R S S L Y R A G G A - - - - - -   LTb
201  - - S Q P - - - - - - - - L S H K V Y M R N F K - - - - - -   FASL.pep
202  - - N Q P - - - - - - - - L N H K V Y M R N S K - - - - - -   FAS LIGAND  U06948.pep
 61  S Q E N E I A E R S F R T L P H I S L L A E I K T V S F Q T   HTPAN08XX.SEQ.FULL.pep
122  - - P K A P S S P L Y - - L A H E V Q L F S S Q - - - - - -   HUMAN TNF BETA   M55913.pep

                    400              410              420
111  - - - - - - - - - - - - - - Y P E P T Q - - L L M G T R S V C E   HUVE091.pep
163  - - - - - - - - - - - - - - Y Q T K V N - - L L S A I K S P C Q   TNFa.pep
142  - - - - - - - - - - - - - - Y P F H V P - - L L S S Q K M V Y P   TNFb
170  - - - - - - - - - - - - - - Y G P G T P E L L L E G A E T V T P   LTb
215  - - - - - - - - - - - - - - Y P G D L V - - L M E E K K L N Y C   FASL.pep
216  - - - - - - - - - - - - - - Y P E D L V - - L M E E K R L N Y C   FAS LIGAND  U06948.pep
391  L M Q W L T S S V F I I Y S L R L K K A Q Q S I S Q V V Y H   HTPAN08XX.SEQ.FULL.pep
142  - - - - - - - - - - - - - - Y P F H V P - - L L S S Q K M V Y P   HUMAN TNF BETA   M55913.pep

                    430              440              450
127  V G S - - - - - - - - - - - - N - - - - - - - - - - - - W F   HUVE091.pep
179  R E T - - - - - - - - - - - - P E - - G A E A K P - - - W Y   TNFa.pep
158  - - - - - - - - - - - - - - - - G L Q E P - - - W L   TNFb
188  V L D - - - - - - - - - - - P A R R Q G Y G P L - - - W Y   LTb
231  - - - - - - - - - - - - - - - T T G Q I - - - W A   FASL.pep
232  - - - - - - - - - - - - - - - T T G Q I - - - W A   FAS LIGAND  U06948.pep
421  S S S L Q V S L R D N I L K S K E R R G T T K R S Q F A W C   HTPAN08XX.SEQ.FULL.pep
158  - - - - - - - - - - - - - - - G L Q E P - - - W L   HUMAN TNF BETA   M55913.pep
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                        460              470                480
 33  Q P I Y L G A M F S L Q E - - - - - - - - - - - - - G D K L M   HUVEO91.pep
192  E P I Y L G G V F Q L E K - - - - - - - - - - - - - G D R L S   TNFa.pep
165  H S M Y H G A A F Q L T Q - - - - - - - - - - - - - G D Q L S   TNFb
203  T S V G F G L V Q L R R - - - - - - - - - - - - - G E R V Y   LTb
238  H S S Y L G A V F N L T V - - - - - - - - - - - - - A D H L Y   FASL.pep
239  H S S Y L G A V F N L T S - - - - - - - - - - - - - A D H L Y   FAS LIGAND  U06948.pep
451  S G S H L S Q H F G N P R W V D H E I K R S R P P T N P I S   HTPAN08XX.SEQ.FULL.pep
165  H S M Y H G A A F Q L T Q - - - - - - - - - - - - - G D Q L S   HUMAN TNF BETA   M55913.pep

                        490              500                510
151  V N V S D I S L V D Y - - - - - - - - T K E D K T F - - -   HUVEO91.pep
210  A E I N R P D Y L D F - - - - - - - - A E S G Q V Y - - -   TNFa.pep
183  T H T D G I P H L V L - - - - - - - - S - P S T V F - - -   TNFb
221  V N I S H P D M V D F - - - - - - - - A R - G K T F - - -   LTb
256  V N I S Q L S L I N F - - - - - - - - E - E S K T F - - -   FASL.pep
257  V N I S Q L S L I N F - - - - - - - - E - E S K T F - - -   FAS LIGAND  U06948.pep
481  T E S A K I S W V C W H M P V V P A T E A E A G E S F E P G   HTPAN08XX.SEQ.FULL.pep
183  T H T D G I P H L V L - - - - - - - - S - P S T V F - - -   HUMAN TNF BETA   M55913.pep

                        520              530
169  - - - - - F G A F L - - - - - - - - - - - L           HUVEO91.pep
228  - - - - - F G I I A - - - - - - - - - - - L           TNFa.pep
200  - - - - - F G A F A - - - - - - - - - - - L           TNFb
238  - - - - - F G A V M - - - - - - - - - - - V G         LTb
273  - - - - - F G L Y K - - - - - - - - - - - L           FASL.pep
274  - - - - - F G L Y K - - - - - - - - - - - L           FAS LIGAND  U06948.pep
 11  R Q R L Q C G E I M P L H S S L A T E R D L V         HTPAN08XX.SEQ.FULL.pep
200  - - - - - F G A F A - - - - - - - - - - - L           HUMAN TNF BETA   M55913.pep
```

Decoration 'Decoration #1': Box residues that match the Consensus within 2 distance units.

Human Genome ‾iences, Inc.

Pla‾ .D.(s) _____ _____

Date Initiated: _____

Date Completed: ⟶8·10·94 _____

Results Folder: 08/10/94 22 HGS

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: 22
Prep Person:	Prep Person: ACS	Gel Loader: Alice
Prep Date:	Prep Date: 08/09/94	Run Date: 08/09/94

# 1-A9	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	Edited vector	length	% Nsl	Trash Code
	Rluscript									AANOFF GEL		
2-B9	HLMACO64RPO2	NING/HL	7196									N
3-C9	HLMACO67RPO2	NING/HL	7196									N
4-D9	HLMACO68RPO2	NING/HL	7196									N
5-E9	HPDOM93RP01 ✓	ANN KIM	7439	373	296	153	117	-12.00				P
6-F9	HPDOM93FP02 X	ANN KIM	7479	269	187	114	73	11.06				D
7-G9	HIBEB69RP01 ✓	ANN KIM	7437	178	144	65	83	10.74	40	340		
8-H9	HIBEB69FP02	ANN KIM	7436									N
9-A10	HTPAN08S04FP17 ✓	ANN KIM	7408	460	329	252	156	-12.00				P
10-B10	HTPAN08S04FP18 ✓	ANN KIM	7407	443	306	252	147	-12.00				R
11-C10	HTPAN08S04RP19 ✓	ANN KIM	7406	51	75	53	41	-12.00				R
12-D10	HTPAN08S04RP20 ✓	ANN KIM	7405	683	556	249	252	10.27	20	330		
3-E10	HE9MF73SO5RP16 ✓	ANN KIM	7098	167	218	98	64	10.41	32	330		
14-F10	HE9MF73SO5FP17 ✓	ANN KIM	7105	248	219	172	91	10.38	30	330		
15-G10	HE9MF73SO5RP18 ✓	ANN KIM	7106	212	319	147	117	10.41	30	380		
16-H10	HE9MF73SO5RP19 ✓	ANN KIM	7109	206	377	111	115	10.43	20	400		
17-A11	HE9MF73SO5FP20 ✓	ANN KIM	7128	211	207	134	72	10.46				P
18-B11	HE9MF73SO5RP21 ✓	ANN KIM	7170	272	354	127	190	10.35	50	350		
19-C11	HE9MF73SO5FP22 ✓	ANN KIM	7171	359	293	290	153	10.46	40	390		
20-D11	HE20142RP01 ✓	ANN KIM	6802	307	314	130	112	10.43	10	390		
21-E11	HE20142FP03 ✓	ANN KIM	6986	275	172	111	91	10.32				P
22-F11	HE20142RP05 ✓	ANN KIM	7027	337	332	143	95	10.33	20	400		
23-G11	HETAS76RP02 λ	ANN KIM	6152									N
24-H11	HETAS76RP03 ✓	ANN KIM	7112	273	226	91	110	10.41	20	400		
25-A12	HCEOJ23S30AP02	D.KOZAK	1989	78	49	27	27	10.43	20	400		
26-B12	HCEOJ23S30BP02	D.KOZAK	1989									N
27-C12	HCEOJ23S30CP02	D.KOZAK	1989	65	42	23	23	10.61	20	390		
28-D12	HCEOJ23S30DP02	D.KOZAK	1989	116	62	37	41	10.17	50	371		
29-E12	HCEOJ23S30EP02	D.KOZAK	1989	103	63	35	36	10.46	20	420		
30-F12	HCEOJ23S30FP02	D.KOZAK	1989	46	68	37	38	10.43	20	400		
31-G12	HCEOJ23S30GP02	D.KOZAK	1989	115	73	39	36	10.58	20	430		
32-H12	HCEOJ23S30HP02	D.KOZAK	1989	88	54	20	25	10.55	20	391		

Analyzed by: Dm
Uploaded by: Jm   Folder: SCI / FL

Factura/Blast Analysis: _____

Additional Comments:
19~4/156c @ 13:19

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: _____

Results Folder: 08/10/94 38 HGS

% Good: _____   % Good: _____

	Templates		Sequence Reaction		Gel Run	
Method:		Method:		Machine ID:	38	
Prep Person:		Prep Person:		Gel Loader:	Karen	
Prep Date:		Prep Date:		Run Date:	8/9	

#	Sample Name	Scientist name/init. control	Primer DP/DT for	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	bluescriptF			318	30	171	123	0.63		580		
2	HPRCU93F	Politis		240	158	98	84	10.57	50	200	1	—
3	HTPAN08S04F	A. Kim		283	190	136	115	10.58	50	250	1	—
4	HIBEB69F	A. Kim		145	74	77	57	10.46	20	200	1	—
5	HPDDM93F	A. Kim		59	37	29	28	10.47	20	240	3	—
6	HETAS76F	A. Kim		205	92	112	81	10.47	50	250	1	—
7	HTOAS71Fa	HLA		351	279	119	67	10.53	50	350	1	—
8	HFSBC6533F1	HUDSON							50			—
9	HFSBC6533F2	HUDSON							50			T
10	HFSBC6533F3	HUDSON							50			R
11	HE2PD40AF	D. Kozak										I
12	HILCJ44AF	D. Kozak		128	82	42	39	10.54	50	400	1	—
13	HE2CB95AF	D. Kozak		176	117	68	50	10.63	50	340	1	—
14	bluescript HCEOJ23S30KR	Control	rev									R
15	HT2SA16Ra	RPW										R
16	HCEOJ23S30AR	D.Kozak		106	62	48	37	10.65	95	305	1	—
17	HCEOJ23S30BR	D.Kozak										R
18	HCEOJ23S30CR	D.Kozak		325	196	99	70	10.70	100	450	1	—
19	HCEOJ23S30DR	D.Kozak										N
20	HCEOJ23S30ER	D.Kozak										R
21	HCEOJ23S30FR	D.Kozak										R
22	HCEOJ23S30GR	D.Kozak		228	109	65	55	10.69	100	370	1	—
23	HCEOJ23S30HR	D.Kozak		150	92	56	45	10.69	100	360	1	—
24	HCEOJ23S30IR	D.Kozak		213	146	58	64	10.75	100	340	2	—
25	HCEOJ23S30JR	D.Kozak		100	54	39	38	10.76	95	350	1	—
26	HCEOJ23S30KR bluescript	D.Kozak	B/S	164	101	63	48	10.69	95	360	1	—
27	HCEOJ23S30LR	D.Kozak							98	430		.
28	HCEOJ23S30MR	D.Kozak		109	59	33	32	10.70	100	150		
29	HCEOJ23S30NR	D.Kozak		231	119	68	45	10.74	100	380	1	—
30	HCEOJ23S30OR	D.Kozak		211	108	68	49	10.69	100	360	1	—
31	HCEOJ23S30PR	D.Kozak										R
32	HPRCU93Ra	Politis		495	228	132	108	10.74	100	300	1	—

alyzed by: Kin

uploaded by: Kin Folder: Pt Sci

Additional Comments:

Buffer leak   gel problem

Factura/Blast Analysis: _____

95

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: _____

Results Folder: 08|10|94 39 HGS

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method:	Machine ID: 39
Prep Person:	Prep Person:	Gel Loader: Karen
Prep Date:	Prep Date:	Run Date: 8/9

#	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% N	Trash Code
1-A1	HTPAN08S04R B/S	A KIM	rev	303	418	158	211	10.57		330	3	-
2-B1	HIBEB69R	A KIM		588	26	112	100	10.46	100	330	1	-
3-C1	HPDDM93R	A KIM		266	305	190	39	10.43	100	310	1	-
4-D1	HETAS76R	A KIM		454	301	158	103	10.52	95	390	i	-
5-E1	HFSBC6S33R1	Hudson							95			R
6-F1	HFSBC6S33R2	Hudson		179	166	105	56	10.53	95	305	1	-
7-G1	HFSBC6S33R3	Hudson		194	183	75	60	10.58	95	250	4	
8-H1	HSRDG78R1c	a chopra		391	321	129	127	10.47	90	340	3	-
9-A2	HSRDG78R1d	a chopra		281	341	141	135	10.52	90	360	2	-
10-B2	HSJAF39R1c	a chopra		458	381	164	130	10.49	95	230	2	-
11-C2	HSJAF39R1d	a chopra		690	505	214	203	10.44	95	340	2	-
12-D2	HGBBH79R1c	a chopra	(	236	196	78	81	10.56	95	350	2	-
13-E2	HGBBH79R1d	a chopra		148	116	63	61	10.54	95	380	2	-
14-F2	DNAE02+346R	FISCHER										N
15-G2	DNASE04+346R	FISCHER										N
16-H2	BLUESCRIPT HTPAN08S04	control										R
17-A3												
18-B3												
19-C3												
20-D3												
21-E3												
22-F3												
23-G3												
24-H3												
25-A4												
26-B4												
27-C4												
28-D4												
29-E4												
30-F4												
31-G4												
32-H4												

Kim upload to FL/Sci

96

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____ ✓

Date Initiated: _____

Date Completed: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 14
Prep Person:	Prep Person: karen	Gel Loader: Andrew
Prep Date:	Prep Date: 8/10/94	Run Date: 8/10/94

#	Sample Name	Scientist name/init control	Primer DP/DT FOR	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% Ns	Trash Code
1	bluescriptF		FOR	264	156	69	118	11.90		380		
2	HE2S10F	A KIM	FOR	75	3	17	25	10.22	30	200	2	Primer
3	HE2S11F	A KIM	FOR	291	173	116	11	10.77	45	280	2	SF
4	HE2S12F	A KIM	FOR	202	166	131	56	10.16	41	120	2	
5	HE2S13F	A KIM	FOR	315	251	95	73	10.70	41	270	2	
6	HE2S14F	A KIM	FOR	254	186	163	53	10.74	40	280	1	—
7	HE2S15F	A KIM	FOR	266	254	95	92	10.61	40	260	1	—
8	HE2S16F	A KIM	FOR	—							2	—
9	HE2S17F	A KIM	FOR	—								N
10	HE2S18F	A KIM	FOR	446	335	165	121	10.75	40	330	N	—
11	HE2S19F	A KIM	FOR	340	342	130	142	10.85	40	300	1	—
12	HE2S20F	A KIM	FOR	332	411	176	124	10.69	40	310	1	—
13	HE2S21F	A KIM	FOR	208	208	149	122	10.52	40	230	2	—
14	HE2S22F	A KIM	FOR	405	316	167	145	10.41	45	250	2	—
15	HE2S23F	A KIM	FOR	597	475	140	135	10.56	40	280	2	—
16	HE2S24F	A KIM	FOR	474	434	118	124	10.50	60	300	3	—
17	HE2S25F	A KIM	FOR	425	367	151	126	10.76	50	300	2	—
18	HE2S26F	A KIM	FOR	256	353	123	110	10.59	50	300	3	—
19	HE2S27F	A KIM	FOR	266	225	111	114	10.73	50	300	2	—
20	HE2S28F	A KIM	FOR									R
21	HE2OI42F	A KIM	FOR	45	240	68	124	10.61	40	330	2	—
22	HSUSH20F	A KIM	FOR	223	309	123	116	10.62	50	300	2	—
23	HI8EB69F	A KIM	FOR	313	146	84	54	10.52	20	370	<1	—
24	HPDOM93F	A KIM	FOR	443	354	06	116	10.54	55	375	2	—
25	HE9MF73S05F	A KIM	FOR	571	252	100	106	10.61	50	300	2	—
26	HE9MF73S07F	A KIM	FOR	454	346	114	109	10.49	50	275	2	—
27	HTPAN08S04F	A KIM	FOR	552	433	162	149	10.49	45	325	2	—
28	HTPAN08S13F	A KIM	FOR	613	464	158	146	10.49	40	350	2	—
29	HTPAN08F	A KIM	FOR	732	449	147	132	10.51	40	300	1	—
30	HALSK38F	A KIM	FOR	494	511	204	197	10.52	40	270	1	—
31	HOSAB71F	A KIM	FOR	734	417	174	84	10.53	45	280	2	—
32	HE9MF73F	A KIM	FOR	443	460	138	125	10.41	50	280	2	—

Stacked-IVY

alyzed by: Kim
uploaded by: Kim   Folder: F.L/Sci

Factura/Blast Analysis: _____

Additional Comments:
all looks good,
strong primers

All samples - 11, 12, 13F all had
SF break ~85 bp

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Human Genome Sciences, Inc.

Plate I.D.(s) ___ manuals

Date Initiated: _____

Date Completed: ___ 8/11/94 _____

Results Folder: __ 08/11/94 18 HGS __

% Good: 24/32   % Good: _____

	Templates	Sequence Reaction	Gel Run
Method:		Method: manual	Machine ID: 18
Prep Person:		Prep Person: karen	Gel Loader: Kw
Prep Date:		Prep Date: 8/10/94	Run Date: 8·10

#	Sample Name		Scientist name/init control	Primer DP/DT rev	Signal Strength C	A	G	T	Base Spacing	Vector	Edited Length	% N's	Trash Code
1	bluescriptR		control	rev	200	121	76	68	9.99	101	349	29	
2	HE2S10R	X	A KIM	REV									2
3	HE2S11R	✓	A KIM	REV	258	131	98	81	10.06	99	331	51.5	
4	HE2S12R	✓	A KIM	REV	161	98	65	49	10.04	101	339	1.8	
5	HE2S13R	✓	A KIM	REV	249	141	84	68	10.06	96	364	3.6	
6	HE2S14R	✓	A KIM	REV	171	98	58	46	10.04	101	349	4.0	
7	HE2S15R	✓	A KIM	REV	215	159	82	65	10.05	101	349	1.7	
8	HE2S16R	X	A KIM	REV									
9	HE2S17R	X	A KIM	REV									2
10	HE2S18R	✓	A KIM	REV	273	212	124	106	10.00	100	—		2 I
11	HE2S19R	✓	A KIM	REV	309	226	153	91	10.03	101	—		I
	HE2S20R	✓	A KIM	REV	383	225	118	101	10.04	101	—		I
13	HE2S21R	✓	A KIM	REV	34	238	128	109	9.95	100	320	1.6	
14	HE2S22R	✓	A KIM	REV	476	228	137	115	9.92	101	319	2.2	
15	HE2S23R	✓	A KIM	REV	369	270	141	119	9.95	99	261	9.9	
16	HE2S24R	✓	A KIM	REV	404	255	126	111	9.91	101	319	1.6	
17	HE2S25R	✓	A KIM	REV	29	187	116	96	10.02	100	290	1.0	
18	HE2S26R	✓	A KIM	REV	322	218	130	110	10.00	100	330	1.5	
19	HE2S27R	✓	A KIM	REV	310	203	126	101	9.98	100	330	4.8	only A @43. only A @43.
20	HE2S28R	X MIXED	A KIM	REV	237	170	106	8c	9.82	100	—		I
21	HE2O142R	✓	A KIM	REV	176	122	74	61	9.95	101	408	9.9	
22	HSUSH20R	✓	A KIM	REV	197	125	74	59	10.00	101	319	1.6	
23	HIBEB69R	v. small primer pk	A KIM	REV									N
24	HPDOM93R		A KIM	REV	274	182	104	86	9.93	100	330	0.6	
25	HE9MF73S05R	✓	A KIM	REV	159	115	70	72	10.11	99	371	7.9	
26	HE9MF73S07R	✓	A KIM	REV	197	117	63	62	10.02	101	369	1.4	
27	HTPAN08S04R	✓	A KIM	REV	363	246	135	118	10.07	101	349	2.3	
28	HTPAN08S13R	✓	A KIM	REV	229	140	94	68	10.08	95	315	1.3	
29	HTPAN08R	✓	A KIM	REV	507	366	153	183	9.99	101	269	0.7	
30	HALSK38R	✓	A KIM	REV	297	350	58	57	9.96	95	345	1.2	
31	HOSAB71R	✓	A KIM	REV	393	320	153	117	9.99	102	348	3.7	
32	HE9MF73R	✓	A KIM	REV	503	418	214	152	10.02	96	334	0.6	

reviewed - IVY

Analyzed by: IVY

Uploaded by: IVY   Folder: Full length + scientists   Factura/Blast Analysis: _____

Additional Comments:

98

Human Genome Sciences, Inc.

Plate I.D.(s) _manuals 2_

Date Initiated: _____

Date Completed: **8-18-94**

Results Folder: **08|18|94 40 H66**

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method: MISC.	Method: MANUAL/BIOMEK	Machine ID: 40
Prep Person: MISC.	Prep Person: SMR	Gel Loader: ASP
Prep Date: MISC.	Prep Date: 08/17/94	Run Date: 08/17/94

#	Sample Name	Scientist name/init.	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	bluescript	control	REV	258	149	104	87	10.10	~20	370	4N/11	
2-B5	HHPSI21R	soppet/g	rev									N
3-C5	HPRAE75R	soppet/g	rev	434	326	147	130	10.07	92	358	4n/16	
4-D5	HMNAD13CR	ANN KIM	rev	103	65	37	31	9.90	100	141	3n/14	
5-E5	HMNAD13DR	ANN KIM	rev	219	135	66	48	10.02	95	305	4n/16	
6-F5	HTPBY11CR	ANN KIM	rev	63	48	31	32	9.81	103	210	11n/56	
7-G5	HPTBY11DR HTPBY11DR	ANN KIM	rev	79	63	33	35	9.79	100	230	4n/56	
8-H5	HLTBR89AR	ANN KIM	rev	543	338	145	148	10.02	97	369	4n/	
9-A6	HLTBR89BR	ANN KIM	rev	423	299	166	141	10.01	96	336	1n/	
10-B6	HLTBA03AR	ANN KIM	rev	462	382	198	182	9.95	97	359	4n/14	
11-C6	HLTBA03BR	ANN KIM	rev	380	372	174	155	9.76	95	345	3n/	
2-D6	HSUDK13AR HCSDK	ANN KIM	rev	448	331	191	162	9.87	99	341	5n/16	
13-E6	HSUDK13BR HCSDK	ANN KIM	rev	596	374	236	213	9.92	94	349	7n/36	
14-F6	HTTCI56AR	ANN KIM	rev	510	378	190	151	9.83	100	260	3n/56	
15-G6	HTTCI56BR	ANN KIM	rev	238	225	102	71	9.88	100	300	2N/6	
16-H6	HMSBZ43AR	ANN KIM	rev	524	405	230	199	9.91	94	321	100n/56	
17-A7	HMSBZ43BR	ANN KIM	rev	480	361	215	191	9.92	103	303	14n/51	
18-B7	HE2FF12R	D.Kozak	revers	258	217	100	86	9.87	97	340	5n/11	
19-C7	HAFAD33AR	D.Kozak	revers	156	123	171	47	9.89	96	342	4n/61	
20-D7	HAFAD33BR	D.Kozak	revers	28	103	52	46	9.93				P, R
✓ 21-E7	HE6CL09Rdmso	MING	REV	224	185	116	102	9.75	97	—	—	
✓ 22-F7	HE6CL68Rdmso	MING	REV	90	123	92	82	7.79		—	—	
✓ 23-G7	HE6CL96Rdmso	MING	REV	206	130	87	82	9.79	100	—	n	
24-H7	PSK SP6	control	SP6	135	107	110	45	-12	99	—	M	
25-A8	TTS-AT	PFY		103	86	119	47	9.91		—	—	R
26-B8	TTS-BT			81	47	96	35	9.95		380	2%	
27-C8	TTS-CT			85	110	102	48	10.09		340	3%	
28-D8	P-ETR015	↓	↓	15	87	68	27	10.03		440	1%	
29-E8										—		u
30-F8												
31-G8												
32-H8												

Analyzed by: **DND/JSS**

loaded by: **ASP**   Folder: **Full length + scientists**

Factura/Blast Analysis: _____

Additional Comments: **Retracked-y**
✓=SFS

99

Human Genome Sciences, Inc.

Plate I.D.(s) ___manuals 1___

Date Initiated: _____

Date Completed: ___8/18/94___

Results Folder: ___05/18/94 35 HGS___

% Good: _____   % Good: ___88%___

Templates	Sequence Reaction	Gel Run
Method:MISC	Method:BIOMEK/MANUAL	Machine ID: 35
Prep Person:MISC	Prep Person: SMR	Gel Loader: ASP
Prep Date:MISC	Prep Date: 8/17/94	Run Date: 8/17/94

#	Sample Name	Scientist name/init	Primer DF/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% N	Trash Code
1-A1	bluescript	control	for	361	222	162	134	10.19	~40	410	>1	
2-B1	HPFDL91Fa	jian Ni	for	81	56	42	30	9.95	~50	350	>1	
3-C1	HUNAE76Fa	jian Ni	for	58	37	34	28	10.01				
4-D1	HE9CF32Fa	jian Ni	for	41	40	29	21	10.00				T
5-E1	HE8AS10Fa	jian Ni	for	79	47	44	47	9.99	~70			T
6-F1	HHPSI21F	soppet/g	for									T
7-G1	HPRAE75F	soppet/g	for	206	173	66	97	9.86	50	350	>1	N
8-H1	HMNAD13CF	ANN KIM	for	130	81	41	57	9.91	50	330	>1	
9-A2	HMNAD13DF	ANN KIM	for	152	234	172	129	10.07	50	330	1.5	
10-B2	HTPBY11CF	ANN KIM	for	97	72	40	30	9.80	50	350	>1	
11-C2	HPTBY11BF HT?BY11DF	ANN KIM	for	110	76	46	34	9.78	50	310	>1	
12-D2	HLTBR89AF	ANN KIM	for	428	374	199	120	9.80	50	370	>1	
13-E2	HLTBR89BF	ANN KIM	for	508	317	215	125	9.81	50	400	>1	
14-F2	HLTBA03AF	ANN KIM	for	394	262	222	198	9.81	40	590	0	
15-G2	HSUDK13AF HCSDK	ANN KIM	for	346	368	148	146	9.80	50	400	>1	
16-H2	HLTBA03BF	ANN KIM	for	279	326	88	116	9.83	50	370	>1	
17-A3	HSUDK13BF HCSDK	ANN KIM	for	503	353	256	132	9.81	50	400	1.2	
18-B3	HTTCI56AF	ANN KIM	for	457	372	159	97	9.73	50	360	3.0	
19-C3	HTTCI56BF	ANN KIM	for	220	200	81	55	9.71	40	400	1.5	
20-D3	HMS8Z43AF	ANN KIM	for	420	379	201	111	9.76	40	290	4.1	
21-E3	HMS8Z43BF	ANN KIM	for	738	471	273	164	9.80	50	390	>1	
22-F3	CNB8PG2	KOVACS	for	60	44	32	23	9.79	~60	230	1.7	
23-G3	CNB8PG3	KOVACS	for	257	213	81	88	9.88	~10	470	>1	
24-H3	CNB8PG4	KOVACS	for	338	365	110	145	9.75	~20	300	3.6	
25-A4	CNB8PG5	KOVACS	for	298	179	152	95	9.83	~50	400	2.5	
26-B4	CNB8PG6	KOVACS	for	348	220	143	119	9.79	~70	360	1.9	
27-C4	CNB8PG7	KOVACS	for	465	203	161	145	9.81	~90	350	>1	
28-D4	CNB8PG8	KOVACS	for	328	198	154	119	9.79	~10	500	>1	
29-E4	bluescript	control	rev	269	217	104	89	9.84	95	300	>1	
30-F4	LAP4RA	JPW	rev	178	143	84	30	9.83	100	320	>1	
31-G4	LAP4RB	JPW	rev	139	115	70	64	9.89	100	270	>1	
32-H4	LAP4RC	JPW	rev	160	114	78	65	9.85	98	280	>1	

Analyzed by: ___ASP___

loaded by: ___ASP___   Folder: ___Full length + scientists___

Factura/Blast Analysis: _____

Additional Comments: ___Retracted ___

100

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

'ate Initiated: _____

Date Completed: _____

Results Folder: _8·19.94 17HG?4_

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manuals	Machine ID: 1 7
Prep Person:	Prep Person: karen	Gel Loader:renee
Prep Date:	Prep Date: 8/18/94	Run Date:8/18/94

#	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	HSUSH20S13RP01	ANN KIM	6800	28	53	85	52	9.00		310		
2-B1	HSUSH20S14RP01	ANN KIM	6800	31	56	90	55	9.00		350		
3-C1	HSUSH20S15RP01	ANN KIM	6800	87	159	231	117	9.00		380		
4-D1	HSUSH20S16RP01	ANN KIM	6800	98	86	149	77	9.00		340		
5-E1	HSUSH20S17RP01	ANN KIM	6800	27	42	67	52	9.00		290		
6-F1	HSUSH20S18RP01	ANN KIM	6800	20	31	40	42	9.00		290		
7-G1	HSUSH20S19RP01	ANN KIM	6800	17	28	42	35	9.00		290		
8-H1	HSUSH20S20RP01	ANN KIM	6800	14	19	26	35	-12.00		290		
9-A2	HSUSH20S21RP01	ANN KIM	6800	53	94	137	107	9.00		355		
10-B2	HSUSH20S22RP01	ANN KIM	6800	29	46	53	75	9.00		350		
11-C2	HSUSH20S23RP01	ANN KIM	6800	46	93	125	100	9.00		390		
12-D2	HSUSH20S24RP01	ANN KIM	6800	27	41	43	36	9.00		360		
13-E2	HSUSH20S25RP01	ANN KIM	6800	33	35	33	28	-7.00				R
14-F2	HSUSH20S13FP04	ANN KIM	6987	64	111	155	127	9.00		460		
15-G2	HSUSH20S14FP04	ANN KIM	6987	32	52	71	51	9.00		350		
16-H2	HSUSH20S15FP04	ANN KIM	6987	91	116	194	162	9.00		310		
17-A3	HSUSH20S16FP04	ANN KIM	6987	54	139	173	164	9.00		350		
18-B3	HSUSH20S17FP04	ANN KIM	6987	61	95	61	55	9.00		380		
19-C3	HSUSH20S18FP04	ANN KIM	6987	23	35	43	73	-12.00		300		
20-D3	HSUSH20S19FP04	ANN KIM	6987	34	18	47	75	9.00		340		
21-E3	HSUSH20S20FP04	ANN KIM	6987	13	12	18	44	-7.00				R
22-F3	HSUSH20S21FP04	ANN KIM	6987	65	115	160	112	9.00		390		
23-G3	HSUSH20S22FP04	ANN KIM	6987	21	39	46	57	9.00		340		
24-H3	HSUSH20S23FP04	ANN KIM	6987	36	101	105	16	9.00		330		
25-A4	HSUSH20S24FP04	ANN KIM	6987	36	73	73	85	9.00		350		
26-B4	HSUSH20S25FP04	ANN KIM	6987	77	41	43	76	9.00		290		
27-C4	HSUSH20RP01B	ANN KIM	6800	65	126	189	135	9.00		410		
28-D4	HSUSH20FP04	ANN KIM	6987	48	78	123	99	9.00		480		
29-E4	HTPAN08S04RP01d	ANN KIM	685	85	255	29	29	9.00		330		
30-F4	HTPAN08S04RP03d	ANN KIM	5424	74	303	308	902	9.00		380		
31-G4	HTPAN08S04RP05d	ANN KIM	5426	46	391	115	136			290		
32-H4	BLUESCRIPTDT	CONTROL		52	96	137	138	9.00		450		

.nalyzed by: PYS

Uploaded by: eye Folder: _FL/SS._

Factura/Blast Analysis: _____

Additional Comments:

Bluescript : 8/3/94

DT RXN MIX : 848-003

TIPS : 40628433

Silent Monitor : 099311

Tubes : P16J4

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Results Folder: 8-19-94 18 HGS

Date Completed: _____

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 18
Prep Person:	Prep Person: karen	Gel Loader: renee
Prep Date:	Prep Date: 8/18/94	Run Date: 8/18/94

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	HTPAN08S04RPO6d	ANN KIM	5676	90	355	296	79	6.00		370		
2-B5	HTPAN08S04RPO7d	ANN KIM	5688	81	273	30	447	9.00		250		
3-C5	HTPAN08S04RP10d	ANN KIM	6442	53	420	29	250	9.00		350		
4-D5	HTPAN08S04RP12d	ANN KIM	6638	32	508	213	203	9.00		296		
5-E5	HTPAN08S04RP14d	ANN KIM	6640	130	38	377	347	9.00		348		
6-F5	HTPAN08S04FP15d	ANN KIM	6813	52	148	73	63	70.00				R
7-G5	HTPAN08S04FP16d	ANN KIM	7409	105	296	341	204	9.00		270		
8-H5	HTPAN08S04FP17d	ANN KIM	7408	153	323	361	590	9.00		300		
9-A6	HTPAN08S04FP118d	ANN KIM	7407	86	213	296	149	9.00		380		
10-B6	HTPAN08S04RP19d	ANN KIM	7406	83	26	18	235	9.00		375		
11-C6	HTPAN08S04RP20d	ANN KIM	7405	34	433	29	172	9.00		390		
12-D6	HTCC156ARP01	ANN KIM	685	45	50	118	163	9.00		290		
13-E6	HTCC156ARP03	ANN KIM	5424	59	213	209	359	-1200				R
14-F6	HTCC156ARP05	ANN KIM	5426	51	373	144	34	9.00		245		
15-G6	HTCC156ARP06	ANN KIM	5676	211	251	108	122	9.00		168		
16-H6	HTCC156ARP07	ANN KIM	5688	55	171	190	271	9.00		120		
17-A7	HTCC156ARP10	ANN KIM	6442	59	274	126	136	9.00		300		
18-B7	HTCC156ARP12	ANN KIM	6638	90	160	239	266	9.00		236		
19-C7	HTCC156ARP14	ANN KIM	6640	100	109	296	335	0.00		260		
20-D7	HTCC156AFP15	ANN KIM	6813	43	110	136	213	-1200				R
21-E7	HTCC156AFP16	ANN KIM	7409	70	167	123	155	9.00		296		
22-F7	HTCC156AFP17	ANN KIM	7408	46	59	91	129	9.00		300		
23-G7	HTCC156AFP18	ANN KIM	7407	411	113	108	178	9.00		300		
24-H7	HTCC156ARP19	ANN KIM	7406	77	481	161	266	9.00		270		
25-A8	HTCC156ARP20	ANN KIM	7405	66	33	210	232	-1200		340		
26-B8	HOSDK13ARP03	ANN KIM	5424	88	304	286	155	9.00		357		
27-C8	HOSDK13ARP07	ANN KIM	5688	64	201	249	159	9.00		150		
28-D8	HOSDK13AFP15	ANN KIM	6813	37	75	95	167	9.00		280		
29-E8	HOSDK13ARP19	ANN KIM	7406	111	500	190	333	0.00		310		
30-F8	HOSDK13ARP20	ANN KIM	7405	119	65	311	30	9.00		270		
31-G8	bluescriptDT	CONTROL		51	103	117	137	9.00		380		
32-H8												

analyzed by: PYS

Uploaded by: PYS   Folder: FL/SS

Factura/Blast Analysis: _____

Additional Comments:

Bluescript: 8/3/94

RXN Mix: 848-003

Tips 40628433

Silent Monitor: 099-311

Tubes: P1654

102

Human Genome Sciences, Inc.

Plate i.D.(s) _____ _____

Date Initiated: _____

Date Completed: _____

Results Folder: 8-19-94 18 HGS

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 18
Prep Person:	Prep Person: karen	Gel Loader: renee
Prep Date:	Prep Date: 8/18/94	Run Date: 8/18/94

#	Sample Name	Scientist name/init	Primer DP/DT	C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	HTPAN08S04RP06d	ANN KIM	5676	9c	305	246	39	9.00		30		
2-B5	HTPAN08S04RP07d	ANN KIM	5688	51	273	307	447	9.00		280		
3-C5	HTPAN08S04RP10d	ANN KIM	6442	8.3	420	29	250	9.00		350		
4-D5	HTPAN08S04RP12d	ANN KIM	6638	72	608	23	253	9.00		240		
5-E5	HTPAN08S04RP14d	ANN KIM	6640	130	28	377	367	9.00		378		
6-F5	HTPAN08S04FP15d	ANN KIM	6813	62	148	173	63	72.00				L
7-G5	HTPAN08S04FP16d	ANN KIM	7409	105	376	344	304	9.00		270		
8-H5	HTPAN08S04FP17d	ANN KIM	7408	153	393	361	597	9.00		200		
9-A6	HTPAN08S04FP118d	ANN KIM	7407	86	273	216	4?	9.00		320		
10-B6	HTPAN08S04RP19d	ANN KIM	7406	8.3	269	148	55	9.00		375		
11-C6	HTPAN08S04RP20d	ANN KIM	7405	38	433	29	172	9.00		380		
2-D6	HTCCI56ARP01	ANN KIM	685	45	39	173	163	9.00		240		
13-E6	HTCCI56ARP03	ANN KIM	5424	59	273	309	339	-12.00				L
14-F6	HTCCI56ARP05	ANN KIM	5426	51	393	144	74	9.00		345		
15-G6	HTCCI56ARP06	ANN KIM	5676	211	351	108	122	9.00		168		
16-H6	HTCCI56ARP07	ANN KIM	5688	55	17	190	271	9.00		120		
17-A7	HTCCI56ARP10	ANN KIM	6442	57	274	156	176	9.00		300		
18-B7	HTCCI56ARP12	ANN KIM	6638	90	160	239	246	9.00		236		
19-C7	HTCCI56ARP14	ANN KIM	6640	100	109	24?	338	9.00		260		
20-D7	HTCCI56AFP15	ANN KIM	6813	43	110	134	213	72.00				L
21-E7	HTCCI56AFP16	ANN KIM	7409	70	167	123	155	9.00		298		
22-F7	HTCCI56AFP17	ANN KIM	7408	48	59	91	39	9.00		300		
23-G7	HTCCI56AFP18	ANN KIM	7407	41	113	108	78	9.00		300		
24-H7	HTCCI56ARP19	ANN KIM	7406	77	48	161	266	9.00		270		
25-A8	HTCCI56ARP20	ANN KIM	7405	86	33	310	28	-12.00		380		
26-B8	HOSDK13ARP03	ANN KIM	5424	88	32	086	55	9.00		357		
27-C8	HOSDK13ARP07	ANN KIM	5688	64	361	349	459	9.00		150		
28-D8	HOSDK13AFP15	ANN KIM	6813	37	75	95	167	9.00		280		
29-E8	HOSDK13ARP19	ANN KIM	7406	111	580	190	373	9.00		310		
30-F8	HOSDK13ARP20	ANN KIM	7405	119	615	311	352	9.00		270		
31-G8	bluescriptDT	CONTROL		51	103	117	137	9.00		380		
32-H8												

Analyzed by: RYS

Uploaded by: RYS   Folder: FL/SS

Factura/Blast Analysis: _____

Additional Comments:
Bluescript: 8/3/94
Run Mix: 848-003
Tips 406 28433

Silent Monitor: 099-311
Tubes: P1654

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Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Templates	Sequence Reaction	Gel Run
Method:	Method: manual	Machine ID: 18
Prep Person:	Prep Person: karen	Gel Loader: renee
Prep Date:	Prep Date: 8/18/94	Run Date: 8/18/94

#	Sample Name	Scientist name/init.	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A5	HTPAN08S04RP06d	ANN KIM	5676	9C	55	296	29	6.00		37		
2-B5	HTPAN08S04RP07d	ANN KIM	5688	51	273	30	447	9.00		280		
3-C5	HTPAN08S04RP10d	ANN KIM	6442	53	420	29	250	9.00		350		
4-D5	HTPAN08S04RP12d	ANN KIM	6638	22	508	23	273	9.00		240		
5-E5	HTPAN08S04RP14d	ANN KIM	6640	130	208	377	347	9.00		348		
6-F5	HTPAN08S04FP15d	ANN KIM	6813	52	148	78	163	72.00				R
7-G5	HTPAN08S04FP16d	ANN KIM	7409	105	376	244	204	9.00		270		
8-H5	HTPAN08S04FP17d	ANN KIM	7408	153	323	341	597	9.00		300		
9-A6	HTPAN08S04FP118d	ANN KIM	7407	86	253	246	42	9.00		300		
10-B6	HTPAN08S04RP19d	ANN KIM	7406	83	249	78	55	9.00		375		
11-C6	HTPAN08S04RP20d	ANN KIM	7405	58	453	29	172	9.00		380		
2-D6	HTCCI56ARP01	ANN KIM	685	45	50	118	163	9.00		290		
13-E6	HTCCI56ARP03	ANN KIM	5424	59	213	209	359	-12.00				R
14-F6	HTCCI56ARP05	ANN KIM	5426	51	373	144	74	9.00		345		
15-G6	HTCCI56ARP06	ANN KIM	5676	211	251	108	122	9.00		168		
16-H6	HTCCI56ARP07	ANN KIM	5688	55	176	190	271	9.00		120		
17-A7	HTCCI56ARP10	ANN KIM	6442	59	274	136	176	9.00		300		
18-B7	HTCCI56ARP12	ANN KIM	6638	90	610	237	236	9.00		236		
19-C7	HTCCI56ARP14	ANN KIM	6640	100	109	246	338	9.00		260		
20-D7	HTCCI56AFP15	ANN KIM	6813	43	110	136	213	-12.00				R
21-E7	HTCCI56AFP16	ANN KIM	7409	70	167	123	155	9.00		290		
22-F7	HTCCI56AFP17	ANN KIM	7408	42	59	51	179	9.00		300		
23-G7	HTCCI56AFP18	ANN KIM	7407	41	113	123	178	9.00		300		
24-H7	HTCCI56ARP19	ANN KIM	7406	77	451	161	266	9.00		270		
25-A8	HTCCI56ARP20	ANN KIM	7405	61	332	210	222	-12.00		390		
26-B8	HOSDK13ARP03	ANN KIM	5424	55	33	286	55	9.00		327		
27-C8	HOSDK13ARP07	ANN KIM	5688	64	201	249	459	9.00		130		
28-D8	HOSDK13AFP15	ANN KIM	6813	32	55	95	167	9.00		280		
29-E8	HOSDK13ARP19	ANN KIM	7406	111	550	190	255	0.00		310		
30-F8	HOSDK13ARP20	ANN KIM	7405	114	65	311	50	9.00		270		
31-G8	bluescriptDT	CONTROL		51	103	117	137	9.00		380		
32-H8												

Human Genome Sciences, Inc.

Plate I.D.(s) _____ _____

Date Initiated: _____

Date Completed: **8-20-94**

Results Folder: **08/20/94   39   HGS**

% Good: _____   % Good: _____

Templates	Sequence Reaction	Gel Run
Method: MISC	Method: BIOMEK/MANUAL	Machine ID: **39**
Prep Person: MISC	Prep Person: SMR/**ASP**	Gel Loader: **ASP**
Prep Date: MISC	Prep Date: 08/19/94	Run Date: **8/19/94**

#	Sample Name	Scientist name/init	Primer DP/DT	Signal Strength C	A	G	T	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	bluescript	Control	for	147	227	154	158	9.37	70	430	3%/6	
2-B1	HOSAA69F	HLI	FOR	271	135	151	116	9.23	—			R
3-C1	HOSAA70F	HLI	FOR	174	137	71	53	9.31	—			T
4-D1	HOSAA71F	HLI	FOR	111	134	63	41	9.30	76	146	5%	
5-E1	HMEDM76F	HLI	FOR	37	41	24	21	9.28				R
6-F1	HTTCA40AF	ANN KIM	for	94	124	41	49	9.34	70	425	6%/1%	
7-G1	HTTCA40BF	ANN KIM	for	267	834	70	144	9.33	70	409	5%/1%	
8-H1	bluescript	Control	rev	166	240	114	123	9.42	93	305	13%/4%	
9-A2	HCEBM41Ra	Kunsch	REV	158	168	79	70	9.40	93	357	4%/1%	
10-B2	HCEBM41Rb	Kunsch	REV	339	249	120	103	9.35	93	337	3%/1%	
11-C2	HOSAA69R	HLI	REV	113	135	87	80	9.52	93			
2-D2	HOSAA70R	HLI	REV	142	126	77	69	9.46	95			R
13-E2	HOSAA71R	HLI	REV	151	141	51	65	9.41	95	255	4%/1%	L
14-F2	rpb3ra	paul	REV	373	292	156	140	9.45	92			
15-G2	he2cb95ra	paul	REV	152	621	277	332	9.35	92	268	3%/1%	M
16-H2	hhpft46ra	paul	REV	258	198	95	105	9.39	93	347	4%/1%	
17-A3	httck42ra	paul	REV	—								
18-B3	hhfbt61ra	paul	REV	520	298	204	166	9.36	93	340	2%/1%	N
19-C3	H32EQ28R	soppet/g	REV	443	353	161	159	9.35	93	387	4%/1%	
20-D3	HHF8D38R	soppet/g	REV	402	267	174	165	9.34	95	353	8%/1%	
21-E3	HETBV89R	soppet/g	REV	648	443	243	200	9.41	93	357	4%/1%	
22-F3	HTTCA40AR	ANN KIM	REV	77	77	36	37	9.31	100	325	4%/1%	
23-G3	HTTCA40BR	ANN KIM	REV	413	378	182	113	9.34	92	338	2%/1%	
24-H3	bluescript	Control	rev	356	249	126	144	9.41	92	325	6%/1%	
25-A4												
26-B4												
27-C4												
28-D4												
29-E4												
30-F4												
31-G4												
32-H4												

Analyzed by: _____

Uploaded by: _____ Folder: _Full length/Scientists_

Factura/Blast Analysis: _____

Additional Comments:

105

Synthesis Order - 7689 HTPAN08 5'BAM HI

Run date: 8/30/94
Run ID: 7689
Customer: ANN KIM

1.
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7689 HTPAN08 5'BAM HI
Sequence: CCGCG CGG ATC CAC CAT GGC T~~~~~AT GAT GGA GGT C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

[handwritten annotations:]

GCC A/G CC ATG E
   -3 T   +4

G GA TCC GCC CCC
           A

w/ ATG Site from
     Clone

Comments:
Sent to "Synthesizer-2" col 1 seq 31 at 8/31/94 9:58 AM.

[handwritten at bottom:]

G CC ATC
    G
    G/
GCC ATC

G GA TCC ATC ATG
 Bam   Kozak   m

Applied Biosystems

Synthesis Order - 7690 HTPAN08 3'ASP 718

Run date: 8/30/94
Run ID: 7690
Customer: ANN KIM

1.
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 7690 HTPAN08 3'ASP 718
Sequence: GCG CGG TAC CAG TTA GCC AAC TAA AAA GGC CCC G

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
Sent to "Synthesizer-2" col 2 seq 32 at 8/31/94 9:59 AM.

including Stop + Additional Seq.

TAA

Human Genome ~iences, Inc.

Pl~ .D.(s) _____ _____

Date Initiated: _____

Date Completed: _09-13-94_

Results Folder: _09·13·94 23 HGS_

% Good: _____ % Good: _____

Templates	Sequence Reaction	Gel Run
Method:	Method: MANUAL	Machine ID: _23_
Prep Person:	Prep Person: GRP	Gel Loader: _JJm_
Prep Date:	Prep Date: 09/12/94	Run Date: _09·12·94_

#	Sample Name	Scientist name/init. control	Primer DP/DT	Signal Strength G	A	G	C	Base Spacing	vector	Edited length	% Ns	Trash Code
1-A1	BLUESCRIPT			242	156	56	76	10.01	20	440		
2-b1	htaac10s23fp23	fischer										N
3-C1	htaac10s03fp23	fischer										N
4-D1	HTAAC10S02RP29	FISCHER										N
5-E1	HTAAC10S48RP25	FISCHER										N
6-F1	HTAAC10S57RP26	FISCHER										N
7-G1	HTAAC10S01RP28	FISCHER										N
8-H1	HTAAC10S03RP24	FISCHER		100	638	155	46	9.86	60	330		
9-A2	hjuaa13206	paul		159	153	57	55	9.89	10	410		
10-B2	hjuaa13233	paul		142	103	45	39	9.90	10	330		
11-C2	hjuaa13490	paul		163	96	55	35	9.92	30	320		
12-D2	hjuaa13491	paul		223	147	66	53	9.89	30	410		
13-E2	HTPAN08B0SRP05A	ANN KIM		222	254	100	46	9.90	10	340		
14-F2	HTPAN08B0SRP06A	ANN KIM		154	173	72	37	9.95	30	300		
15-G2	HTPAN08B03RP05A	ANN KIM		192	232	90	40	9.90	20	400		
16-H2	HTPAN08B03RP06A	ANN KIM		207	212	90	45	9.95	30	340		
17-A3	HTPAN08B03FP14A	ANN KIM		158	110	76	37	9.91	30	400		
18-B3	HTPAN08B03FP14A	ANN KIM		158	129	99	42	9.86	30	420		
19-C3	HTPAN08B04RP06A	ANN KIM		175	201	105	44	9.73	50	340		
20-D3	HTPAN08B04RP10A	ANN KIM		137	152	55	32	9.80	50	330		
21-E3	HTPAN08B01RP06A	ANN KIM		175	167	72	36	9.84	20	370		
22-F3	HTPAN08B01FP14A	ANN KIM		218	145	91	49	9.87	20	400		
* 23-G3	HTPAN08B02RP06A	FISCHER ANN										N
24-H3	HTPAN08B02RP10A	FISCHER		131	143	59	30	9.87	20	360		
* 25-A4	HTAAC10S01FP23A	FISCHER		179	170	92	66	9.70	40	380		
* 26-B4	HTAAC10S57FP23A	FISCHER		165	110	70	60	9.85	30	410		
27-C4	HSSNB01S01RP07A	KUNSCH		264	174	67	77	9.95	60	300		
28-D4	HSSNB01S01RP08A	KUNSCH		310	253	55	133	9.89	40	320		
* 29-E4	HATBG78RP23A	ZHEN LI		169	121	65	55	9.75	20	400		
30-F4	HPLBQ88RP01fA	HLA		275	204	79	82	9.94	30	340		
31-G4	HPLBQ88FP01fA	HLA		235	103	75	77	-12.00				R
32-H4	HPLBQ88FP01iA	HLA		116	52	41	37	10.16	50	340		

Analyzed by: _JJm_

Uploaded by: _JJm_ Folder: _FL/SC1_

Factura/Blast Analysis: _____

* bluescript vol.(4/e2)

108

Applied Biosystems

Synthesis Order - 2499 HTPAN08S04 3' XBA

Run date: 9/26/94
Run ID: 2499
Customer: ANN KIM

1.   CX
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: HTPAN08S04 3'XBA - PD10
Sequence: GCG AGA TCT CAG TTA GCC AAC TAA AAA GGC CCC GAA

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Sent to "Synthesizer-2" col 1 seq 31 at 9/27/94 7:01 AM.

109

Applied Biosystems
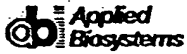
Synthesis Order - 2500 HTPAN08S04 5'BAM HI

Run date: 9/26/94
Run ID: 2500
Customer: ANN KIM

1.   CX
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: HTPAN08S04 5' BAM HI -PD10
Sequence: GGG GGA TTC AAG CAG ATG CAG GAC AAG TAC TCC AAA

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:
 Sent to "Synthesizer-2" col 2 seq 32 at 9/27/94 7:02 AM.

Applied Biosystems

Synthesis Order - 2656 htpan08s04 3'xba

Run date: 10/26/94
Run ID: 2656 AMK
Customer: a kim

1.   KH
2.
Synthesizer: Synthesizer-2
Model: 394-08
ROM version: 2.00

Sequence name: 2656 htpan08s04 3'xba
Sequence: CGC GCG AGA TCT CAG TTA GCC AAC TTA AAA GGC C

Cycle: 40 nM CE

End procedure: End CESS
DMT: Off

Comments:

Synthesis Order – 2751 htpan08s04 5'bam new

Run date: 11/7/94
Run ID: 2751 AMK
Customer: a kim

1.   CRG
2.
Synthesizer: None
Model:
ROM version:

Sequence name: htpan08s04 5'bam new
Sequence: GCG GCG GGA TCC ATG GGC TAT GAT GGA GGT CCA

Cycle:

End procedure:
DMT: Off

Comments:

SYNTHESIZED ON 3948

Translate DNA Sequence htpan08 185bporf(1,714)
With Standard Genetic Code

Molecular Weight 27689.30 Daltons
237 Amino Acids
31 Strongly Basic(+) Amino Acids (K,R)
30 Strongly Acidic(-) Amino Acids (D,E)
65 Hydrophobic Amino Acids (A,I,L,F,W,V)
79 Polar Amino Acids (N,C,Q,S,T,Y)

7.857 Isolectric Point
1.842 Charge at PH 7.0

Total number of bases translated is 714
% A = 34.59
% G = 21.43
% T = 25.07
% C = 18.91
% Ambiguous 0.00

% A+T = 59.66
% C+T = 43.98

Davis,Botstein,Roth Melting Temp C. 80.74
Wallace Temp C   2274.00

Codon usage:

codon	aa	#		codon	aa	#		codon	aa	#		codon	aa	#
acg	( )	0	#	gau	Asp(D)	2	#	---	Ilu(I)	15	#	uca	Ser(S)	3
ccg	( )	0	#	---	Asp(D)	11	#	cua	Leu(L)	1	#	ucc	Ser(S)	5
cgg	( )	0	#	ugc	Cys(C)	1	#	cuc	Leu(L)	3	#	ucu	Ser(S)	7
gcg	( )	0	#	ugu	Cys(C)	2	#	cug	Leu(L)	3	#	---	Ser(S)	26
uag	( )	0	#	---	Cys(C)	3	#	cuu	Leu(L)	1	#	uaa	Ter(.)	1
ucg	( )	0	#	caa	Gln(Q)	9	#	uua	Leu(L)	2	#	---	Ter(.)	1
uga	( )	0	#	cag	Gln(Q)	4	#	uug	Leu(L)	7	#	aca	Thr(T)	6
---	( )	0	#	---	Gln(Q)	13	#	---	Leu(L)	17	#	acc	Thr(T)	3
gca	Ala(A)	2	#	gaa	Glu(E)	14	#	aaa	Lys(K)	9	#	acu	Thr(T)	1
gcc	Ala(A)	2	#	gag	Glu(E)	5	#	aag	Lys(K)	8	#	---	Thr(T)	10
gcu	Ala(A)	4	#	---	Glu(E)	19	#	---	Lys(K)	17	#	ugg	Trp(W)	5
---	Ala(A)	8	#	gga	Gly(G)	3	#	aug	Met(M)	6	#	---	Trp(W)	5
aga	Arg(R)	9	#	ggc	Gly(G)	3	#	---	Met(M)	6	#	uac	Tyr(Y)	6
agg	Arg(R)	2	#	ggg	Gly(G)	5	#	uuc	Phe(F)	3	#	uau	Tyr(Y)	7
cga	Arg(R)	1	#	ggu	Gly(G)	2	#	uuu	Phe(F)	7	#	---	Tyr(Y)	13
cgc	Arg(R)	1	#	---	Gly(G)	13	#	---	Phe(F)	10	#	gua	Val(V)	2
cgu	Arg(R)	1	#	cac	His(H)	3	#	cca	Pro(P)	1	#	guc	Val(V)	3

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---	Arg(R)	14	#	cau	His(H)	3	#	ccc	Pro(P)	3	#	gug	Val(V)	1
aac	Asn(N)	7	#	---	His(H)	6	#	ccu	Pro(P)	3	#	guu	Val(V)	4
aau	Asn(N)	7	#	aua	Ilu(I)	6	#	---	Pro(P)	7	#	---	Val(V)	10
---	Asn(N)	14	#	auc	Ilu(I)	3	#	agc	Ser(S)	3	#	nnn	???(X)	0
gac	Asp(D)	9	#	auu	Ilu(I)	6	#	agu	Ser(S)	8	#	TOTAL		238

```
           10        20        30        40
    ....l....l ....l....l ....l....l ....l....l
    MQDKYSKSGI ACFLKEDDSY WDPNDEESMN SPCWQVKWQL 40
    RQLVRKMILR TSEETISTVQ EKQQNISPLV RERGPQRVAA 80
    HITGTRGRSN TLSSPNSKNE KALGRKINSW ESSRSGHSFL 120
    SNLHLRNGEL VIHEKGFYYI YSQTYFRFQE EIKENTKNDK 160
    QMVQYIYKYT SYPDPILLMK SARNSCWSKD AEYGLYSIYQ 200
           210       220       230       240
    ....l....l ....l....l ....l....l ....l....l
    GGIFELKEND RIFVSVTNEH LIDMDHEASF FGAFLVG. 238
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Translate DNA Sequence htpan08orf(1,846)
With Standard Genetic Code

Molecular Weight 32511.50 Daltons
281 Amino Acids
32 Strongly Basic(+) Amino Acids (K,R)
32 Strongly Acidic(-) Amino Acids (D,E)
84 Hydrophobic Amino Acids (A,I,L,F,W,V)
94 Polar Amino Acids (N,C,Q,S,T,Y)

7.324 Isolectric Point
0.784 Charge at PH 7.0

Total number of bases translated is 846
% A = 32.27
% G = 22.81
% T = 25.06
% C = 19.86
% Ambiguous 0.00

% A+T = 57.33
% C+T = 44.92

Davis,Botstein,Roth Melting Temp C. 81.80
Wallace Temp C   2750.00

Codon usage:

codon	AA	#		codon	AA	#		codon	AA	#		codon	AA	#
acg	( )	0	#	gau	Asp(D)	2	#	---	Ilu(I)	17	#	uca	Ser(S)	3
ccg	( )	0	#	---	Asp(D)	11	#	cua	Leu(L)	1	#	ucc	Ser(S)	5
cgg	( )	0	#	ugc	Cys(C)	2	#	cuc	Leu(L)	5	#	ucu	Ser(S)	8
gcg	( )	0	#	ugu	Cys(C)	3	#	cug	Leu(L)	7	#	---	Ser(S)	28
uag	( )	0	#	---	Cys(C)	5	#	cuu	Leu(L)	1	#	uaa	Ter(.)	1
ucg	( )	0	#	caa	Gln(Q)	9	#	uua	Leu(L)	2	#	---	Ter(.)	1
uga	( )	0	#	cag	Gln(Q)	8	#	uug	Leu(L)	7	#	aca	Thr(T)	7
---	( )	0	#	---	Gln(Q)	17	#	---	Leu(L)	23	#	acc	Thr(T)	5
gca	Ala(A)	2	#	gaa	Glu(E)	14	#	aaa	Lys(K)	9	#	acu	Thr(T)	2
gcc	Ala(A)	2	#	gag	Glu(E)	7	#	aag	Lys(K)	9	#	---	Thr(T)	14
gcu	Ala(A)	6	#	---	Glu(E)	21	#	---	Lys(K)	18	#	ugg	Trp(W)	5
---	Ala(A)	10	#	gga	Gly(G)	5	#	aug	Met(M)	9	#	---	Trp(W)	5
aga	Arg(R)	9	#	ggc	Gly(G)	3	#	---	Met(M)	9	#	uac	Tyr(Y)	8
agg	Arg(R)	2	#	ggg	Gly(G)	6	#	uuc	Phe(F)	4	#	uau	Tyr(Y)	7
cga	Arg(R)	1	#	ggu	Gly(G)	2	#	uuu	Phe(F)	8	#	---	Tyr(Y)	15
cgc	Arg(R)	1	#	---	Gly(G)	16	#	---	Phe(F)	12	#	gua	Val(V)	3
cgu	Arg(R)	1	#	cac	His(H)	3	#	cca	Pro(P)	1	#	guc	Val(V)	4

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			#				#				#			
---	Arg(R)	14	#	cau	His(H)	3	#	ccc	Pro(P)	4	#	gug	Val(V)	6
aac	Asn(N)	8	#	---	His(H)	6	#	ccu	Pro(P)	3	#	guu	Val(V)	4
aau	Asn(N)	7	#	aua	Ilu(I)	6	#	---	Pro(P)	8	#	---	Val(V)	17
---	Asn(N)	15	#	auc	Ilu(I)	5	#	agc	Ser(S)	4	#	nnn	???(X)	0
gac	Asp(D)	9	#	auu	Ilu(I)	6	#	agu	Ser(S)	8	#	TOTAL		282

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          10         20         30         40
 .....|....| .....|....| .....|....| .....|....|
MAMMEVQGGP SLGQTCVLIV IFTVLLQSLC VAVTYVYFTN 40
ELKQMQDKYS KSGIACFLKE DDSYWDPNDE ESMNSPCWQV 80
KWQLRQLVRK MILRTSEETI STVQEKQQNI SPLVRERGPQ 120
RVAAHITGTR GRSNTLSSPN SKNEKALGRK INSWESSRSG 160
HSFLSNLHLR NGELVIHEKG FYYIYSQTYF RFQEEIKENT 200

         210        220        230        240
 .....|....| .....|....| .....|....| .....|....|
KNDKQMVQYI YKYTSYPDPI LLMKSARNSC WSKDAEYGLY 240
SIYQGGIFEL KENDRIFVSV TNEHLIDMDH EASFFGAFLV 280
G. 282
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                        10        20        30        40        50        60
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP16(1>164) <-  CTTAAGGATGATTGRCCAGAA-TCTCTGATTCTGTAGCACATGACTNACTTGCTAGACAT
HTPAN08P185RP50(1>226) ->          ACTCGCAAATAAATAAGTATTTTACTGTGTTCGTA-ACAG
                           CTTAAGGATGATTGACCAGAA-TCGCAAATAAAGAAGCACATGACTGACTTCCTA-ACAG


                        70        80        90        100       110       120
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP16(1>164) <-  GGWTGTTG-AAGCCAGACCTATCGAGACCCYGGWAGATGCATAMCCTCY-A-GAYWTCGG
HTPAN08P185RP50(1>226) ->  TGTTGTAATAAAAAA-ACCTATRAATATTCCGGATTATTCATACCGTCCCACCA--TCGG
HTPAN08P185FP14(1>338) <-              GGWAGATGCATAMCCTCY-A-GAYTTCGG
HTPAN08P185FP08(1>388) <-                     ATGCATAACCTCT-AAGACWTCGG
                           GGTTGTAA-AAAAAA-ACCTATCAAGACCCCGGAAGATGCATAACCTCC-A-GACTTCGG


                        130       140       150       160       170       180
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP16(1>164) <-  GGTTGGAT-CCATCATGCAGGACAAGTACTCCAAMAGTGNCATTGCTTG
HTPAN08P185RP50(1>226) ->  GGGCGGAT-CCATCATGSAGGACAAGTNCTCCAAAAGTGGTATTGCTTGTTTCTTAATAG
HTPAN08P185FP14(1>338) <-  GSGTGGAT-CCATCATGCAGGACAAGTACKCCMCCAGTGGCATTGCTTGTTTYTTAAAAG
HTPAN08P185FP08(1>388) <-  GGKTGGATCCCATCATGCAGGACAAGTACTCCAAAAGTGNCATTGCTTGTTTCGTAAAAG
htpan08 185bporf(1>714)->          ATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAG
                           GGGTGGAT-CCATCATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAG


                        190       200       210       220       230       240
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP50(1>226) ->  AGGATGACAGYTATTGGGACCCC-AATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAA
HTPAN08P185FP14(1>338) <-  AAGATGACAGTTATTGGGACCCC-AATGACGAAGAGAGTATGGACAGCCCCTGCTGGCAA
HTPAN08P185FP08(1>388) <-  AAGATGACAGTTATTGGGACCCCCAATGACGAAGAGAGTATGAACARCCCCTKCTGRCAA
htpan08 185bporf(1>714)->  AAGATGACAGTTATTGGGACCCC-AATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAA
                           AAGATGACAGTTATTGGGACCCC-AATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAA


                        250       260       270       280       290       300
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP50(1>226) ->  TGTCAAGTGGCA
HTPAN08P185FP14(1>338) <-  -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC
HTPAN08P185FP08(1>388) <-  -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC
htpan08 185bporf(1>714)->  -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC
                           -GTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAAC


                        310       320       330       340       350       360
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP14(1>338) <-  CATTTCTACAGTTCAAGRAAAGCAACCMAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC
HTPAN08P185FP08(1>388) <-  CATTTCTACAGTTCAAGAAAAGCAACCAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC
htpan08 185bporf(1>714)->  CATTTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC
                           CATTTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCC


                        370       380       390       400       410       420
                 ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP14(1>338) <-  TCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGGAGAAGCAACACATTSTCTTCTCC
HTPAN08P185FP08(1>388) <-  TCAGAGAGTAGCACCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCC
htpan08 185bporf(1>714)->  TCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCC
                           TCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCC
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                            430       440       450       460       470       480
                        ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP14(1>338) <-  AMACTCCAAGAATG
HTPAN08P185FP08(1>388) <-  AAACTCCAAGAATGAAAAGGCTCTGGRCCGCMAAATAAACTCCTGCGAATCATCAAGGAG
htpan08 185bporf(1>714)->  AAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAG
                           AAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGCGAATCATCAAGGAG

                            490       500       510       520       530       540
                        ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185FP08(1>388) <-  TGG-CAT
htpan08 185bporf(1>714)->  TGGGCATTCATTCCTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAA
HTPAN08P185RP05(1>391) ->                        AAGAGGAATGGTGACCTGGTCATCCATGAAAA ...
                           TGG-CATTCATTCCTGAGCAACTTGCACAAGAGGAATGGTGAACTGGTCATCCATGAAAA

                            550       560       570       580       590       600
                        ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->  AGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAA
HTPAN08P185RP05(1>391) ->  AGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAA
HTPAN08P185FP17(1>259) ->                                                             A
                           AGGGTTTTACTACATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAA

                            610       620       630       640       650       660
                        ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->  CACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCC
HTPAN08P185RP05(1>391) ->  CACAAAGAACGACAAACAAATGGYCCAATATATTTACAAATACACAAGTTATCCTGACCC
HTPAN08P185FP17(1>259) ->  CACAAGGAACGACACCCAN-TGGTCCAATATATTTACAAATACACAAGTTATCCTGACCC
                           CACAAAGAACGACAAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCC

                            670       680       690       700       710       720
                        ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->  TATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACT
HTPAN08P185RP05(1>391) ->  TATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACT
HTPAN08P185FP17(1>259) ->  TATATTGTGGATGAAAAGTGCTAGAAATAGTKGTTGGTCTAAAGATGCAGAATATGGACT
                           TATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACT

                            730       740       750       760       770       780
                        ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->  CTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTC
HTPAN08P185RP05(1>391) ->  CTATTCCATCTATCARGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTKTGTTTC
HTPAN08P185FP17(1>259) ->  CTATYCCATCTATCAAGGGGGAATWTTKGAGCTTAAGGAAAATGACAGAATTTTTGGTTTC
HTPAN08P185RP06(1>271) ->                                                           TC
                           CTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTC

                            790       800       810       820       830       840
                        ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->  TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
HTPAN08P185RP05(1>391) ->  TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
HTPAN08P185FP17(1>259) ->  TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTYCGGGGCCTTTTT
HTPAN08P185RP06(1>271) ->  TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
                           TGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTT
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                              850       860       870       880       890       900
                         ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08 185bporf(1>714)->  AGTTGGCTAA
HTPAN08P185RP05(1>391) ->  AGTTGGCTAAGCTCTAGATWCGCKCTTWWGGYTCCATCCCCRGAGATSATGTGCTCCAS
HTPAN08P185FP17(1>259) ->  AGTTGGYTAAGCTCTAGAT
HTPAN08P185RP06(1>271) ->  AGTTGGCTAAGCTCTAGATWCSCTCTWT-GGTTCCAT-CCCAGAGATCATRTGCTCCATW
                           AGTTGGCTAAGCTCTAGATACGCTCTTT-GGTTCCAT-CCCAGAGATCATGTGCTCCATA


                              910       920       930       940       950       960
                         ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP06(1>271) ->  GGTGRGATTGGTYRTYCCTCAACTGGAGTTGAGAGWTATTGGTGACCCCATTGGYGAAGW
                           GGTGAGATTGGTCATCCCTCAACTGGAGTTGAGAGATATTGGTGACCCCATTGGCGAAGA


                              970       980       990      1000      1010      1020
                         ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08P185RP06(1>271) ->  GAGTGTKAAYAGCCCCTGCTGGGAARYCAWGTTGAACYTCMGTCAGCWCGTTAGMAAGAT
                           GAGTGTGAACAGCCCCTGCTGGGAAACCAAGTTGAACCTCAGTCAGCACGTTAGAAAGAT


                             1030      1040      1050
                         ....|....|....|....|....|....|.
HTPAN08P185RP06(1>271) ->  SATTTGGATACMCTCTGTGGAACMCATTCAT
                           CATTTGGATACACTCTGTGGAACACATTCAT
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                               10        20        30        40        50        60
                          ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  CACTCGCAAATAATAAGTATTTTACTGTTTTCGTAACAGTGTGGTAATAAAAAAAACCTAT
HTPAN08PA51FP16(1>238)<-                                             ACNCNAACCTAT

                          CACTCGCAAATAATAAGTATTTTACTGTTTTCGTAACAGTGTGGTAATAAAAAAAACCTAT


                               70        80        90       100       110       120
                          ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  AAATATTCCGGATTATTCATACCGCCCCACCATCGGGCGCGGATCCATCATGGNTATGAT
HTPAN08PA51FP16(1>238)<-  ARATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCATCATGTCTATGAT
htpan08orf(1>846)      ->                                               ATGGCTATGAT

                          AAATATTCCGGATTATTCATACCGCCCCACCATCGGGCGCGGATCCATCATGGCTATGAT


                               130       140       150       160       170       180
                          ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  GGAGGTCCAGGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT
HTPAN08PA51FP16(1>238)<-  GGAGGTCCAGGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT
htpan08orf(1>846)      ->  GGAGGTCCAGGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT
HTPAN08PA51FP14(1>416)<-                               CCTGCGTGCTGATCGTGATCTTCACAGT

                          GGAGGTCCAGGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAGT


                               190       200       210       220       230       240
                          ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  GCTCCTGNAGTCTCTCTGTGTGGNTGTAACTTACGTGTACTTTACCAACGAGCTGAAGSA
HTPAN08PA51FP16(1>238)<-  GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA
htpan08orf(1>846)      ->  GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA
HTPAN08PA51FP14(1>416)<-  GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA
HTPAN08PA51FP08(1>389)<-                                             AACGAGCTGAAGCA
HTPAN08PA51RP12(1>371)->                                              CCAACGAGCTGAAGCA

                          GCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCA


                               250       260       270       280       290       300
                          ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  GATGSAGGAC-AARTW-CTCCAAAAGTGGCATTGSTTGTTTCTTAAAAGAAGATGACAGT
HTPAN08PA51FP16(1>238)<-  GATGCAGGAC-AAGTA-CTCCMMCAGTGACATTGCTTGTTTCTT
htpan08orf(1>846)      ->  GATGCAGGAC-AAGTA-CTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT
HTPAN08PA51FP14(1>416)<-  GATGCAGGAC-AAGTA-CTCCMMAAGTGGCATTGCTTGTTTCTTRARAGAAGATGACAGT
HTPAN08PA51FP08(1>389)<-  GATGCAGGACCAAGTACCTCCAAAAGTGGCATTGCTTGTTTCGTAAAAGAAGATGACAGT
HTPAN08PA51RP12(1>371)->  GATGCAGGAC-AAGTA-CTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT
HTPAN08PA51RP10(1>339)->                                       GTTTGTTTCTTAAAAGAAGATGACAGT

                          GATGCAGGAC-AAGTA-CTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT


                               310       320       330       340       350       360
                          ....|....|....|....|....|....|....|....|....|....|....|....|
HTPAN08PA51RP50(1>355)->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGGTGGCAAGTCAAGTGG
htpan08orf(1>846)      ->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51FP14(1>416)<-  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51FP08(1>389)<-  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51RP12(1>371)->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
HTPAN08PA51RP10(1>339)->  TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA

                          TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA
```

120

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                        370       380       390       400       410       420
                       ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)     -> CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
HTPAN08PA51FP14(1>416)<- CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
HTPAN08PA51FP08(1>389)<- CTCCGTCAGMTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT
HTPAN08PA51RP12(1>371)-> CTCCGTCAGCTCGTTAGAAAGATGATTKTGRGAACCTCTGAGGAAACCATTTCTACAGYT
HTPAN08PA51RP10(1>339)-> CTCCGTCAGCTCGTTAGAAAGATGATTTGGAGAACCTCTGAGGAAACCATTTCTACAGTT
                         CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT

                        430       440       450       460       470       480
                       ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)     -> CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51FP14(1>416)<- CAAGAAAAGCAACMAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51FP08(1>389)<- CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51RP12(1>371)-> CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
HTPAN08PA51RP10(1>339)-> CAAGAAAAGCAACAAAATTATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA
                         CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA

                        490       500       510       520       530       540
                       ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)     -> GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51FP14(1>416)<- GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51FP08(1>389)<- GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51RP12(1>371)-> GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT
HTPAN08PA51RP10(1>339)-> GCTCACATAACTGGGACCAGAGGAAGAAGMAACACATTGTCTTCTCCAAACTCCAAGAAT
                         GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT

                        550       560       570       580       590       600
                       ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)     -> GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTC
HTPAN08PA51FP14(1>416)<- GAGAAGNCTCTGGGCCGC
HTPAN08PA51FP08(1>389)<- GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCA
HTPAN08PA51RP12(1>371)-> GAAAAGGCTCTKGGCCSCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCA
HTPAN08PA51RP10(1>339)-> GAAAAGGSTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGSATTCATTC
                         GAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTC

                        610       620       630       640       650       660
                       ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)     -> CTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC
HTPAN08PA51RP10(1>339)-> CTGAGCAACTTG
HTPAN08PA51RP05(1>329)->                     ATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC
                         CTGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTAC

                        670       680       690       700       710       720
                       ....|....|....|....|....|....|....|....|....|....|....|....|
htpan08orf(1>846)     -> ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
HTPAN08PA51RP05(1>329)-> ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
HTPAN08PA51FP17(1>223)->                                             ACAAAGAACGAG
                         ATCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
```

121

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                      730       740       750       760       770       780
               .....l....l....l....l....l....l....l....l....l....l....l....l
htpan08orf(1>846)       ->  AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
HTPAN08PA51RP05(1>329)->    AAACAAATGGYCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
HTPAN08PA51FP17(1>223)->    ACCCACCTGAACCAATATTTTTACAAATACACAAGTTATCCTGACCCTATATTGTGGATG
                            AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG


                      790       800       810       820       830       840
               .....l....l....l....l....l....l....l....l....l....l....l....l
htpan08orf(1>846)       ->  AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
HTPAN08PA51RP05(1>329)->    AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
HTPAN08PA51FP17(1>223)->    AAAAGTGCTAGAAATAGTKGTKGGYCTAAAGATGMAGNCCNNGGACTCTATTCCATCTAT
                            AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT


                      850       860       870       880       890       900
               .....l....l....l....l....l....l....l....l....l....l....l....l
htpan08orf(1>846)       ->  CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
HTPAN08PA51RP05(1>329)->    CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTNTGTTTCTGTAACAAATGAG
HTPAN08PA51FP17(1>223)->    CAAGGGGGAATATTGGAGCTTAAGGAAAATGACAGAATTTNGGTTTCTGTAACAAATGAG
HTPAN08PA51RP06(1>219)->                                               TTTCTGTAACAAATGAG
                            CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG


                      910       920       930       940       950       960
               .....l....l....l....l....l....l....l....l....l....l....l....l
htpan08orf(1>846)       ->  CACTTGATAGACATGG-ACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAA
HTPAN08PA51RP05(1>329)->    CACTTGATAGACATGGCACCGCGAAGCCA
HTPAN08PA51FP17(1>223)->    CACTTGATAGACATGG-ACCGNGAAGCCAG
HTPAN08PA51RP06(1>219)->    CACTTGATAGACATGG-ACCGTGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAAGC
                            CACTTGATAGACATGG-ACCGTGAAGCCAGTTTTTTCGGGGCCTTTTTAGTTGGCTAAGC


                      970       980       990      1000      1010      1020
               .....l....l....l....l....l....l....l....l....l....l....l....l
HTPAN08PA51RP06(1>219)->    TCTAGAAAAGATCTAAGGTACCGATCCAGACATGATAAGATACATTGATGAGTTNGGACA
                            TCTAGAAAAGATCTAAGGTACCGATCCAGACATGATAAGATACATTGATGAGTTXGGACA


                     1030      1040      1050      1060      1070      1080
               .....l....l....l....l....l....l....l....l....l....l....l....l
HTPAN08PA51RP06(1>219)->    AACCACAACTAGAATGCAGNGAAAAAAATGCTTTATTTGTGAAATTNGNGATGCTATTGC
                            AACCACAACTAGAATGCAGXGAAAAAAAATGCTTTATTTGTGAAATTXGXGATGCTATTGC


                     1090
               .....l....l....l....l....
HTPAN08PA51RP06(1>219)->    TTTATTTGGAACCATTAT
                            TTTATTTGGAACCATTAT
```

122

FAS

```
ATGGCTATGATGGAGGTCCAGGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  70
TACCGATACTACCTCCAGGTCCCCCCCTGGGTCGGACCCTGTCTGGACGCACGACTAGCACTAGAAGTGTC

 M  A  M  M  E  V  Q  G  G  P  S  L  G  Q  T  C  V  L  I  V  I  F  T
  W  L  .  W  R  S  R  G  D  P  A  W  D  R  P  A  C  .  S  .  S  S  Q
 N  G  Y  D  G  G  P  G  G  T  Q  P  G  T  D  L  R  A  D  R  D  L  H  S
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+

TGCTCCTGCAGTCTCTCTGTGTGGCTGTAACTTACGTGTACTTTACCAACGAGCTGAAGCAGATGCAGGA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  140
ACGAGGACGTCAGAGAGACACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTCGTCTACGTCCT

 V  L  L  Q  S  L  C  V  A  V  T  Y  V  Y  F  T  N  E  L  K  Q  M  Q  D
  C  S  C  S  L  S  V  W  L  .  L  T  C  T  L  P  T  S  .  S  R  C  R
   A  P  A  V  S  L  C  G  C  N  L  R  V  L  Y  Q  R  A  E  A  D  A  G
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+

CAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGTTATTGGGACCCCAATGACGAA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  210
GTTCATGAGGTTTTCACCGTAACGAACAAAGAATTTTCTTCTACTGTCAATAACCCTGGGGTTACTGCTT

  K  Y  S  K  S  G  I  A  C  F  L  K  E  D  D  S  Y  W  D  P  N  D  E
 T  S  T  P  K  V  A  L  L  V  S  .  K  K  M  T  V  I  G  T  P  M  T  K
  Q  V  L  Q  K  W  H  C  L  F  L  K  R  R  .  Q  L  L  G  P  Q  .  R
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+

GAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAACTCCGTCAGCTCGTTAGAAAGATGATTTTGA
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  280
CTCTCATACTTGTCGGGGACGACCGTTCAGTTCACCGTTGAGGCAGTCGAGCAATCTTTCTACTAAAACT

 E  S  M  N  S  P  C  W  Q  V  K  W  Q  L  R  Q  L  V  R  K  M  I  L
  R  V  .  T  A  P  A  G  K  S  S  G  N  S  V  S  S  L  E  R  .  F  .
 R  E  Y  E  Q  P  L  L  A  S  Q  V  A  T  P  S  A  R  .  K  D  D  F  E
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+

GAACCTCTGAGGAAACCATTTCTACAGTTCAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAG
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  350
CTTGGAGACTCCTTTGGTAAAGATGTCAAGTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTTC

  R  T  S  E  E  T  I  S  T  V  Q  E  K  Q  Q  N  I  S  P  L  V  R  E  R
 E  P  L  R  K  P  F  L  Q  F  K  K  S  N  K  I  F  L  P  .  .  E  K
   N  L  .  G  N  H  F  Y  S  S  R  K  A  T  K  Y  F  S  P  S  E  R  K
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+

AGGTCCTCAGAGAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAAC
+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+  420
TCCAGGAGTCTCTCATCGTCGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTG

  G  P  Q  R  V  A  A  H  I  T  G  T  R  G  R  S  N  T  L  S  S  P  N
 E  V  L  R  E  .  Q  L  T  .  L  G  P  E  E  E  A  T  H  C  L  L  Q  T
  R  S  S  E  S  S  S  S  H  N  W  D  Q  R  K  K  Q  H  I  V  F  S  K
 +----+----+----+----+----+----+----+----+----+----+----+----+----+----+
```

123

```
TCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTCC
--+----+----+----+----+----+----+----+----+----+----+----+----+----+ 490
AGGTTCTTACTTTTCCGAGACCCGGCGTTTTATTTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAGG

   S  K  N  E  K  A  L  G  R  K  I  N  S  W  E  S  S  R  S  G  H  S  F
    P  R  M  K  R  L  W  A  A  K  .  T  P  G  N  H  Q  G  V  G  I  H  S
  L  Q  E  .  K  G  S  G  P  Q  N  K  L  L  G  I  I  K  E  W  A  F  I  P


TGAGCAACTTGCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTACATCTATTCCCA
--+----+----+----+----+----+----+----+----+----+----+----+----+----+ 560
ACTCGTTGAACGTGAACTCCTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATGTAGATAAGGGT

   L  S  N  L  H  L  R  N  G  E  L  V  I  H  E  K  G  F  Y  Y  I  Y  S  Q
    .  A  T  C  T  .  G  M  V  N  W  S  S  M  K  K  G  F  T  T  S  I  P
  E  Q  L  A  L  E  E  W  .  T  G  H  P  .  K  R  V  L  L  H  L  F  P


AACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACAAAGAACGACAAACAAATGGTCCAATATATT
--+----+----+----+----+----+----+----+----+----+----+----+----+----+ 630
TTGTATGAAAGCTAAAGTCCTCCTTTATTTTCTTTTGTGTTTCTTGCTGTTTGTTTACCAGGTTATATAA

    T  Y  F  R  F  Q  E  E  I  K  E  N  T  K  N  D  K  Q  M  V  Q  Y  I
  K  H  T  F  D  F  R  R  K  .  K  K  T  Q  R  T  T  N  K  W  S  N  I  F
   N  I  L  S  I  S  G  G  N  K  R  K  H  K  E  R  Q  T  N  G  P  I  Y


TACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAAAGTGCTAGAAATAGTTGTTGGTCTAAAG
--+----+----+----+----+----+----+----+----+----+----+----+----+----+ 700
ATGTTTATGTGTTCAATAGGACTGGGATATAACAACTACTTTTCACGATCTTTATCAACAACCAGATTTC

   Y  K  Y  T  S  Y  P  D  P  I  L  L  M  K  S  A  R  N  S  C  W  S  K
    T  N  T  Q  V  I  L  T  L  Y  C  .  .  K  V  L  E  I  V  V  G  L  K
  L  Q  I  H  K  L  S  .  P  Y  I  V  D  E  K  C  .  K  .  L  L  V  .  R


ATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTT
--+----+----+----+----+----+----+----+----+----+----+----+----+----+ 770
TACGTCTTATACCTGAGATAAGGTAGATAGTTCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAA

   D  A  E  Y  G  L  Y  S  I  Y  Q  G  G  I  F  E  L  K  E  N  D  R  I  F
    M  Q  N  M  D  S  I  P  S  I  K  G  E  Y  L  S  L  R  K  M  T  E  F
  C  R  I  W  T  L  F  H  L  S  R  G  N  I  .  A  .  G  K  .  Q  N  F


TGTTTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTT
--+----+----+----+----+----+----+----+----+----+----+----+----+----+ 840
ACAAAGACATTGTTTACTCGTGAACTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAA

   V  S  V  T  N  E  H  L  I  D  M  D  H  E  A  S  F  F  G  A  F  L  V
  L  F  L  .  Q  M  S  T  .  .  T  W  T  M  K  P  V  F  S  G  P  F  .  L
   C  F  C  N  K  .  A  L  D  R  H  G  P  .  S  Q  F  F  R  G  L  F  S
```

124

```
GGCTAA
━━━━┿━┿━▶ 846
CCGATT

  G   . .
    A   K
W   L
━━━━━━━▶
```

125

HTPANO8SO4 51bp +PDH
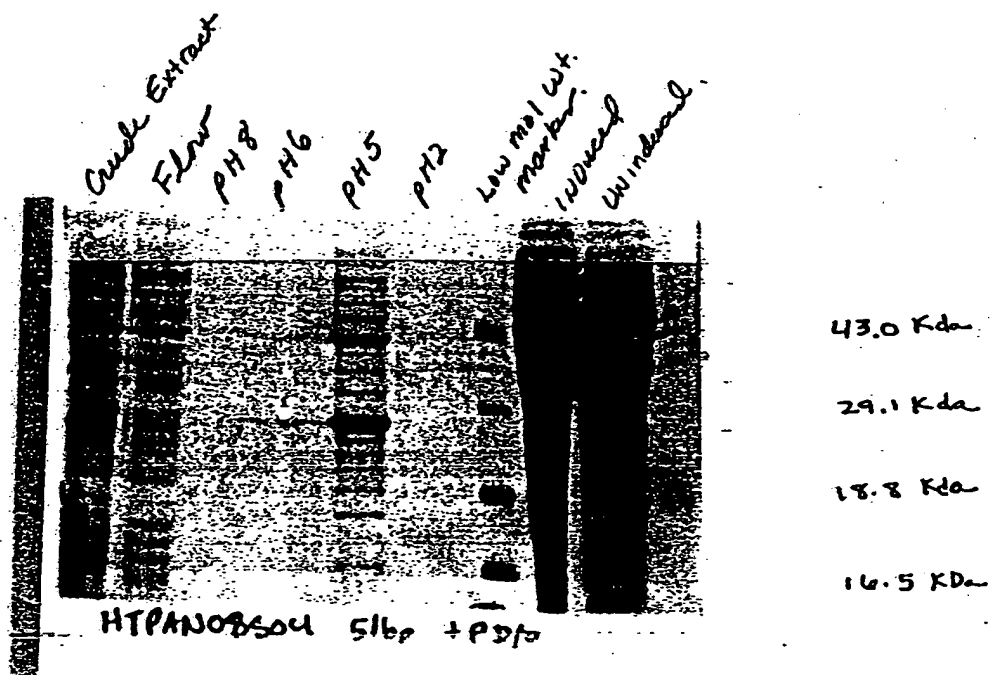
in 6M Gn HCl - ELUTED OVER NiSO4 Column

43.0 Kda

29.1 Kda

18.8 Kda

16.5 KDa
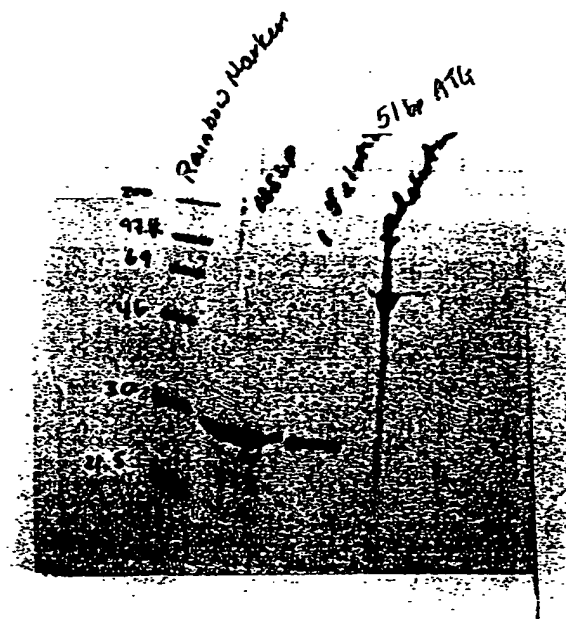
HTPANO8SO4 185bp ATG vs   HTPANO8SO4 51bp ATG
         PH5 elution   1st Elution e 2nd ELUTION IN Immidiol

The TNF Receptor Superfamily
of Cellular and Viral Proteins:
Activation, Costimulation, and Death

Minireview

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Tumor necrosis factor (TNF) seems always to have enjoyed a rather conspicuous visibility in biomedical research. With historical roots in the century-old phenomenon of bacterial-induced hemorrhagic necrosis of tumors, TNF—or, rather, its two homologous forms, TNFα and LTα (lymphotoxin, TNFβ)—were finally molecularly cloned in 1984, among the very first cytokines to be so unambiguously defined. Although TNFα and LTα, classically the respective products of activated macrophages and T cells, can indeed kill many transformed lines, these functionally similar and extraordinarily pleiotropic cytokines are today viewed as primary mediators of immune regulation and the inflammatory response, closely linked to the development of disease. The crucial involvment of TNF, for example, in septic shock, some autoimmune disorders, and graft-host disease is well established (see Beutler, 1992).

Since the cloning of two distinct but structurally homologous receptors for TNF, p75 and p55 (each of which binds both ligands), the past 3 years have witnessed the rapid emergence of two superfamilies, of which the TNFs and their receptors are only representatives (Farrah and Smith, 1992; Suda et al., 1993; Smith et al., 1993). To date, 12 receptors have been identified (Figure 1) with which we can associate some eight TNF-related cytokines (Figure 2). The distinctive but overlapping cellular responses their interactions produce clearly define developmental and regulatory networks involving cells of the lymphoid, hematopoetic, and other lineages. In this minireview we make no attempt to discuss individual members comprehensively and instead highlight emerging global characteristics that distinguish them from other cytokine families: structure, biological networks, and the intriguing ability of some members to induce cell death. A new face to the TNF system seems at hand.

The TNF Receptor Family Interacts
with a Parallel Family of Ligands

The receptors, with two exceptions, are all type I membrane proteins with sequence homology (almost entirely) confined to the extracellular region. The exceptions, T2 and A53R, are poxvirus gene products that map to different genetic loci and have been shown to encode soluble, secreted forms of TNF receptors (Smith et al., 1991). These function to complex (and thereby inactivate) host-produced TNF. T2 is clearly an acquired form of the p75 cellular receptor, while A53R, since it binds only TNFα and shows much lower sequence homology, may represent a third TNF receptor. The extraordinary virulence of wild-type myxoma poxvirus, uniformly fatal to its host (rabbits), is reduced nearly 50% in recombinants differing only by an inactivated T2 gene (Upton et al., 1991). Interestingly,

an intact T2 gene is also conserved in the recently sequenced variola genome, the pathogen responsible for smallpox in humans (Shchelkunov et al., 1993).

The canonical motif of all these receptors is that of cysteine-rich pseudorepeats, each containing about six cysteines and 40 amino acids, although considerable variation in size and number is evident (e.g., CD30 and CD27). Soluble forms, released by proteolysis, for most of these receptors have been observed; one (4-1BB) is generated through alternative splicing (Goodwin et al., 1993). The cytoplasmic domains are rather small (46–221 residues) and generally lack sequence homology among themselves, suggesting major differences in signaling mechanisms. None possess sequences implying catalytic activity.

The ligands for CD30, CD27, CD40, 4-1BB, and Fas were identified and cloned not by protein sequencing, but through direct expression cloning strategies (Goodwin et al., 1993; Suda et al., 1993). This approach rested on the assumption that putative ligands would, like TNFα, exist in active surface forms identifiable by specific binding of soluble receptors (as immunoglobulin fusion chimerics). In fact, all ligands except LTα, which appears to be a secreted protein, reflect prototypic pro-TNFα architecture: type II membrane proteins, with the C-terminus extracellular, the N-terminus intracellular, and a single transmembrane element. Soluble (proteolytically released) forms of TNFα are well known, although reports have not yet established such alternative forms for other ligand members. Family-defining sequence homology (Figure 3) is restricted to ~150 residues in the C-terminal (receptor-
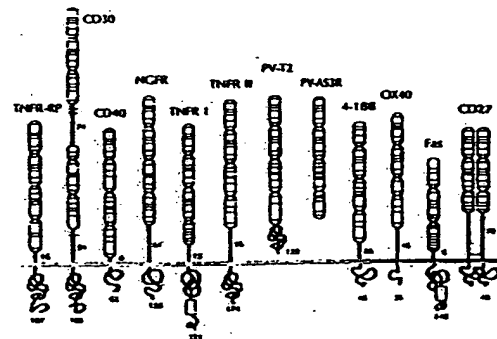
Figure 1. The TNF Receptor Superfamily
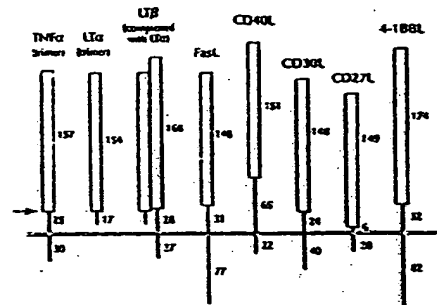
Figure 2. The TNF Family of Cytokines

The homologous C-terminal domains are indicated by open boxes. Extracellular and cytoplasmic domains, which lack sequence homology, are indicated by closed bars. The number of amino acids in each domain is shown. LTα is shown in both secreted and alternative membrane-associated forms, complexed with LTβ. The arrow indicates the proteolytic cleavage site in pro-TNFα that allows for the release of soluble form. Only TNFα, LTα, and LTβ have been shown to form oligomers.

Figure 4. Crystal Structure of Soluble p55 TNFR–LTα Complex
Reprinted from Figure 4 in Banner et al. (1993).

binding) region, which in soluble TNFα and LTα fold into a β-pleated sheet sandwich and trimerize (Eck et al., 1992; Jones et al., 1989). Sequence conservation is particularly high at protomer interfaces. It seems likely, therefore, that all ligands in this family adopt a similar tertiary structure and form oligomers.

A unifying picture of the prototypic interaction between ligands and receptors has literally crystallized from a milestone X-ray diffraction study by Banner et al. (1993), who solved the structure of a human LTα-soluble p55 TNF receptor complex. This complex, containing the extracellular portions of three receptors bound to one LTα trimer, clearly establishes the pseudorepeat sequences in the receptor as true domains forming an elongated array that lies in the interfaces between each pair of the three ligand protomers (Figure 4). Roughly 80% of receptor–ligand contacts occur through domain 2, and each receptor contacts both protomers in the interface. Such a complex would bring receptor cytoplasmic domains into close apposition, presumably complementing binding sites for unknown signaling components, and is consistent with ligand-induced receptor cross-linking as the near universal activation mecha-

nism for growth factors. The novel feature here is that activation involves receptor trimerization; most cytokine families appear to induce dimerization, although by different schemes. Platelet-derived growth factor, for example, is a dimer (immunoglobulin family) whose receptor is a tyrosine kinase, while growth hormone, a member of the hematopoietin family, is a heterodivalent monomer (De Vos et al., 1992).

Many observations, however, suggest this disarmingly simple picture may need revisions. First, structural divergencies in other family members imply variations in interaction motifs. CD30, for example, contains six domains, not four, separated by a nonhomologous region of 74 residues, while CD27 contains three domains, one truncated, and appears to be a disulfide-linked dimer. Further, some evidence suggests that TNFα and LTα oligomers may be intrinsically polydisperse, consisting of homodimers, trimers, and tetramers (Schoenfeld et al., 1990).

Second, one ligand family member (LTβ), with no known biological activity, has been shown to form heterologous complexes with mature LTα (e.g. β2α1), serving to anchor
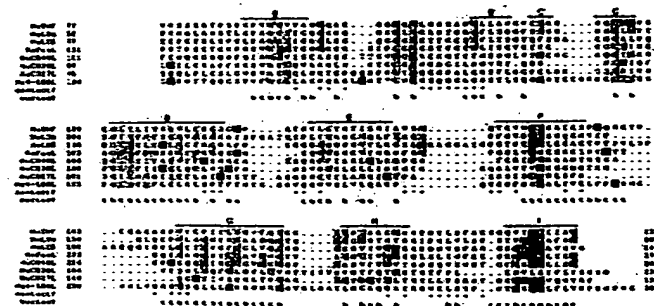
Figure 3. Sequence Homology in C-Terminal Domains of TNF Ligand Family

Alignment begins with N-terminus of soluble TNFα. Residues conserved in four or more members are stippled; cysteines are in closed boxes. Letters B–I indicate β strands in TNF tertiary structure. Asterisks indicate residues having p55 receptor contacts in crystal structure. Lowercase b indicates buried residues in the β-sheet interior; t, residues at TNF protomer-protomer interfaces.

the normally secreted LTα to the cell surface of T, B, and NK cells (Browning et al., 1993). Superficially, these ligands thus begin to resemble cassettes, whereby combinatorial arrangements could produce different oligomers with potentially altered receptor specificities, greatly increasing diversity of function. Such a mechanism in an entirely different family is reflected by the use of the platelet-derived growth factor A and B ligand subunits (A–A, A–B, and B–B dimers) to generate heterotypic and homotypic cross-linked dimers of the α and β receptors. Generic ligand–receptor interactions suggested by the crystal structure of LTα–p55, however, predict that mixed oligomers of LTα–LTβ would produce inactive (that is, ligand-bound but un-cross-linked) p55 (or p75) TNF receptor complexes. This suggests one function of LTβ is to inactivate LTα (with respect to TNF receptors) and implies the existence of a distinct receptor for LTβ that, when cross-linked, would generate novel signals. Heterologous complexes with still other family members could enormously increase the complexity of biological networks.

Third, there is no clear rationale for the redundancy built into the TNFα/LTα (p55/p75) system, nor is it clear how common such redundancies will be in other family members. These ligands display nearly identical biological activities and bind each receptor. Most cells, however, express variable levels of both receptors, even though heterologous receptor cross-links seem prohibited and each receptor can, on its own, transduce different signals (Pfeffer et al., 1993; Tartaglia et al., 1993). One implication is that functional cross-talk may exist between family members.

Fourth, the cytoplasmic domains of these ligands clearly serve important but unknown functions: they are nearly as conserved in sequence across species as extracellular regions, suggesting they carry binding sites for unidentified proteins. For example, we calculate the cytoplasmic domains of human and mouse CD40L are 82% identical; mouse and human TNFα, 86%; mouse and human CD30L, 61%. There is little homology among these domains in different ligands, however, arguing against conservation as a result of common biosynthetic or internalization mechanisms. Since direct cell–cell contact is a primary means of ligand–receptor interaction in this family, bipolar signaling may occur, blurring the distinction between receptor and ligand.

Finally, the low affinity nerve growth factor receptor (NGFR), while structurally a member of this family, binds a family of ligands (the neurotropins) structurally rather different than TNF. NGFR also interacts with the trk family of receptor tyrosine kinases, which show no homology to TNF receptors. Further, while the genomic architectures of CD40, both TNF receptors, and CD27 are rather similar, they appear quite different from the p75 NGFR. Thus, whether the (extracellular) structural homology of NGFR subunit reflects a functional interaction or even distant evolutionary relatedness between these two systems is unclear (Smith et al., 1993). Intriguingly, however, NGF has been shown to affect lymphocyte function. NGFRs are expressed at high levels on follicular dendritic cells in germinal centers, and TNF receptors are expressed on

glial cells of the nervous system, raising the possibility of functional interplay.

Biological Networks: Apoptosis, Necrosis, and Costimulation

Ligand family members can induce pleiotropic biological responses, including differentiation, proliferation, activation, or even cell death. It is clear, however, that T cell–mediated immunity, particularly contact dependent and antigen driven, provides one unifying theme. Without exception, all ligands as well as their receptors are T cell products (although not uniquely so). Both human PBT cells and CD4+ T cell clones show enhanced proliferation when treated with any family ligand in the presence of monoclonal antibodies to CD3 (Goodwin et al., 1993). Thus, autocrine T cell loops, largely mediated through cell–cell contact, are a common feature of the family. The observed variation in ligand induction kinetics is also consistent with different roles for these ligands in T cell activation (Smith et al., 1993; Beutler, 1992). As B cells are also capable of expressing receptors for CD30, CD40, TNFα, LTα, and CD27, for example, this family may contribute T cell help to B cells as well. TNFα and CD30L, however, are also abundantly expressed by activated macrophages, with receptors for the former expressed on nearly all vertebrate cells. Clearly, the dominant physiological networks are an evolving subject.

A consequence of the type II membrane protein architecture of these ligands, particularly on T and B cells, is the cell–cell contact nature of the interaction: it helps ensure ligand expression is antigen dependent and demands that signals generated by TNF family ligands in target cells are productively coordinated with accessory signals generated by other cognate pairs (e.g., cytokine–receptors, CD80–CD28, adhesion molecules such as CD58–CD2). The essence of signaling in this family is therefore one of costimulation. Soluble forms of TNFα (or perhaps CD30L) produced by macrophage may serve to extend the range of activities and provide flexibility to the immune response (Browning et al., 1993; Smith et al., 1993).

The biological function of CD40–CD40L provides a particularly clear example of costimulatory function. Almost exclusively the product of activated CD4+ T cells, CD40L provides essential signals to purified B cells, costimulated with interleukin-4, to undergo immunoglobulin isotype switching and to secrete mature immunoglobulin. Confirmation of this in vitro picture comes from studies of patients carrying mutations in the X-linked CD40L gene: patients show normal numbers of B cells, but a virtual absence of immunoglobulin isotypes other than immunoglobulin M and an inability to mount an antigen-specific antibody response, with concomitant susceptibility to opportunistic infections (Callard et al., 1993).

The TNFα/LTα (p55/p75) system is more complex. Transgenic mice deleted of the p55 TNF receptor illuminate the fundamental importance of TNF and this receptor while illustrating the difficulty in unraveling networks in such a pleiotropic system (Pfeffer et al., 1993). These animals are severely impaired in the clearance of the bacterial pathogen Listeria monocytogenes, die rapidly from infections, and are extraordinarily resistant to lipopolysaccha-

ride-mediated septic shock. Lymphocyte populations, however, are normal and clonal deletion of potentially self-reactive T cells is unimpaired, indicating normal thymocyte development. The creation of p75 TNFR knockout transgenics and, particularly, of double knockouts of p75 and p55 should prove invaluable in dissecting this complex system.

The most recently cloned family member is the Fas ligand, the search for which had approached the status of an immunological Holy Grail (Suda et al., 1993). The reason is that the Fas antigen, broadly expressed on both myeloid and lymphoid cells, including thymocytes, has been characterized as responding to activation (through cross-linking) by inducing apoptotic (programmed) cell death. Since this process is fundamental to immune system development and Ca²⁺-independent T cell–mediated cytotoxicity, the ligand may play a crucial role in these phenomena. This is consistent with the finding that a naturally occurring autosomal recessive mutation in mice, lpr (lymphoproliferation), maps to the fas locus, and homozygous animals exhibit lymphadenapathy and autoimmune disease, resembling systemic lupis in humans. One lpr mutant producing a defective Fas protein behaves as a dominant-negative mutation with respect to a phenotypically very similar mutation, gld (generalized lymphoproliferation disease), on a different chromosome, suggesting that fas and gld encode receptor–ligand cognates (Allen et al., 1990). Nagata and colleagues demonstrate that this is indeed the case (Takahashi et al., 1994 [this issue of Cell]). While defects in the Fas system clearly give rise to aberrancies in the immune system, it seems the proximal cause is not thymic failure to eliminate autoreactive clones through apoptosis, as originally suggested (Watanabe-Fukunaga et al., 1992). Indeed, T cell repertoire formation, as well as both positive and negative selection, proceeds normally in homozygous lpr (or gld) animals (Sidman et al., 1992). Instead, Fas appears to be involved in activation-driven T cell suicide, a process by which chronically activated mature T cells undergo apoptosis, suggesting a role for Fas in peripheral tolerance (Russel and Wang, 1993).

The contingent ability to induce death is rather unique to this family and is well established for TNFα, LTα, and FasL. The p55 TNFR and Fas share a 65 residue homology region in the cytoplasmic domains, which deletion studies have established to be crucial for the apoptotic death activity (Takahashi et al., 1994; Tartaglia et al., 1993). However, Fas appears to have a pleiotropic nature, and it is here that Fas mirrors the properties of other family members. Fresh PBT cells, for example, as well as some B cell tumors, respond to Fas activation with proliferation, not death (Mapara et al., 1993; Alderson et al., 1993). Strikingly similar is the behavior of at least three other family members, CD30 and both TNF receptors. In each case, the specific responses, including cell death (apoptotic or necrotic) or proliferation, depend upon cell type, stage of differention, transformation status, and the presence of other stimuli. Thus, elucidation of the full spectrum of FasL activities may prove unexpectedly illuminating. Their fundamental involvement in the immune system and the window they provide on the apoptosis phenomena, crucial to

many aspects of vertebrate development and homeostasis, combine to ensure ever greater interest in this emerging cytokine family.

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